

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:38:47 ; Search time 938.432 Seconds

(without alignments)
1090.310 Million cell updates/sec

Title: US-10-659-980A-5
Perfect score: 18
Sequence: 1 cccccctctctgcatc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 1641224

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Displaying first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_sts: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_hrg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	18	100.0	18	CQ796912 Sequence
2	18	100.0	18	CS089158 Sequence
3	18	100.0	18	AX316096 Sequence
4	16.4	91.1	18	CS089171 Sequence
5	16.4	91.1	18	AX316109 Sequence
6	14.4	80.0	30	AR083535 Sequence
7	13.8	76.7	18	CQ796928 Sequence
8	13.8	76.7	28	AX191455 Sequence
9	12.8	71.1	17	AR568743 Sequence
10	12.4	68.9	17	BD254227 Sequence
11	12.4	68.9	17	BD254227 Regulatio
12	12.4	68.9	20	CS081520 Sequence
13	12.4	68.9	20	AR311956 Sequence
14	12.2	67.8	17	BD197714 Method an
15	12.2	67.8	23	112779 Sequence 77
16	12.2	67.8	23	AX355960 Sequence
17	12.2	67.8	26	AX922612 Sequence
18	12.2	67.8	27	CS050694 Sequence

C 19	12.2	67.8	30	6	BD107116	BD107116 Monoclonal
C 20	12.2	67.8	30	6	AX205084	AX205084 Sequence
C 21	12.2	67.8	30	6	AX259322	AX259322 Sequence
C 22	12	66.7	17	6	AX27540	AX27540 Sequence
C 23	12	66.7	17	6	AX733930	AX733930 Sequence
C 24	12	66.7	17	6	AX760134	AX760134 Sequence
C 25	12	66.7	18	6	CQ796913	CQ796913 Sequence
C 26	12	66.7	18	6	CS089159	CS089159 Sequence
C 27	12	66.7	18	6	AX316097	AX316097 Sequence
C 28	12	66.7	18	8	HSRTP011	X79751 H. sapiens R
C 29	12	66.7	19	6	AX112294	AX112294 Sequence
C 30	12	66.7	20	6	AR029828	AR029828 Sequence
C 31	12	66.7	20	6	AX298879	AX298879 Sequence
C 32	12	66.7	25	6	AX112272	AX112272 Sequence
C 33	11.8	65.6	17	6	AX734956	AX734956 Sequence
C 34	11.8	65.6	20	6	AR444884	AR444884 Sequence
C 35	11.8	65.6	21	11	CS000256	CS000256 Sequence
C 36	11.8	65.6	23	6	CS088258	CS088258 Sequence
C 37	11.8	65.6	24	6	AR054071	AR054071 Sequence
C 38	11.8	65.6	24	6	AR127460	AR127460 Sequence
C 39	11.8	65.6	25	6	AR239155	AR239155 Sequence
C 40	11.8	65.6	25	6	AX278957	AX278957 Sequence
C 41	11.8	65.6	26	6	AX556664	AX556664 Sequence
C 42	11.6	64.4	18	6	A00428	A00428 Nucleotide
C 43	11.6	64.4	23	6	112780	112780 Sequence 78
C 44	11.6	64.4	24	6	CQ778009	CQ778009 Sequence
C 45	11.6	64.4	25	6	CQ627125	CQ627125 Sequence

ALIGNMENTS

RESULT 1	CQ796912	18 bp	DNA	linear	PAT 19-APR-2004
LOCUS	CQ796912	Sequence 5 from Patent WO2004026772.			
DEFINITION	CQ796912				
ACCESSION	CQ796912.1	GI:46408538			
VERSION	CQ796912.1	GI:46408538			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%;	Score 18;	DB 6;	Length 18;	
Best Local Similarity	100.0%;	Pred. No. 67;			
Matches	18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CCCCCCTCTTCGATAC	18		
Db	1	CCCCCCTCTTCGATAC	18		
RESULT 2	CS089158	18 bp	DNA	linear	PAT 25-MAY-2005
LOCUS	CS089158	Sequence 5 from Patent EP1502948.			
DEFINITION	CS089158				
ACCESSION	CS089158.1	GI:66714442			
VERSION	CS089158.1	GI:66714442			
KEYWORDS					
SOURCE					
synthetic construct					

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 5 02-FEB-2005;
Aguarita Inc. (US)

FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Description of Artificial Sequence: Probe"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTGATAC 18
1 CCCCCCTCTTGATAC 18

Db 1 CCCCCCTCTTGATAC 18

RESULT 3
AXJ16096 18 bp DNA linear PAT 14-DEC-2001
LOCUS AXJ16096
DEFINITION Sequence 5 from Patent WO0190312.
ACCESSION AXJ16096
VERSION AXJ16096.1 GI:17899287
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: WO 0190312-A 5 29-NOV-2001;
AQUARIA, INC. (US)

FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTGATAC 18
1 CCCCCCTCTTGATAC 18

Db 1 CCCCCCTCTTGATAC 18

RESULT 4
CS089171 18 bp DNA linear PAT 25-MAY-2005
LOCUS CS089171
DEFINITION Sequence 18 from Patent EP1502948.
ACCESSION CS089171
VERSION CS089171.1 GI:66714455
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 18 02-FEB-2005;
Aguarita Inc. (US)

FEATURES
source 1..18
Location/Qualifiers

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Primer"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTGATAC 18
1 CCCCCCTCTTGATAC 18

Db 1 CCCCCCTCTTGATAC 18

RESULT 5
AXJ16109 18 bp DNA linear PAT 14-DEC-2001
LOCUS AXJ16109
DEFINITION Sequence 18 from Patent WO0190312.
ACCESSION AXJ16109
VERSION AXJ16109.1 GI:17899300
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: WO 0190312-A 18 29-NOV-2001;
AQUARIA, INC. (US)

FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTGATAC 18
1 CCCCCCTCTTGATAC 18

Db 1 CCCCCCTCTTGATAC 18

RESULT 6
AR083535 30 bp DNA linear PAT 01-SEP-2000
LOCUS AR083535
DEFINITION Sequence 74 from patent US 5976873.
ACCESSION AR083535
VERSION AR083535.1 GI:10010308
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Bohinski, R.J. and White, J.A.
TITLE Nucleic acid sequences controlling lung cell-specific gene
expression
JOURNAL Patent: US 5976873-A 74 02-NOV-1999;
Location/Qualifiers

FEATURES
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCCCCTCTTGATAC 17

RESULT 11
BD254228
LOCUS BD254228 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254228
VERSION BD254228.1 GI:33063998
KEYWORDS JP 2002541795-A/2021.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2021 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2021
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source location/Qualifiers
FT 1.17
/organism='Eukaryote'.
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source location/Qualifiers
1.17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 9.2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCCCTCTCTGGA 15
|||||
1 CCCCTCTCTGGA 14
*
RESULT 12
CQ801520/c
LOCUS CQ801520 20 bp DNA linear PAT 05-MAY-2004
DEFINITION Sequence 30 from Patent WO2004033723.
ACCESSION CQ801520
VERSION CQ801520.1 GI:47058110
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Mitchell, J. and de Bellefiche, J.
TITLE Neurodegenerative disease-associated gene
JOURNAL Patent: WO 2004033723-A 30 22-APR-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source location/Qualifiers
1.20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCCCTCTCTGGA 15
|||||
18 CCCCTCATCTGGA 5
RESULT 13
AR311956
LOCUS AR311956 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2493 from patent US 6559294.
ACCESSION AR311956
VERSION AR311956.1 GI:31705382
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths, R., Hoiseh, S.K., Zagureky, R.J., Metcalf, B.J., Peek, J.A.,
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 2493 06-MAY-2003;
Genet, S.A.;;
FRX;
FEATURES
source location/Qualifiers
1.20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 20;
Best Local Similarity 92.9%; Pred. No. 9.2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CCTCTTCGTGATAC 18
|||||
4 CCTCTTCGTGATTC 17
RESULT 14
BD197714
LOCUS BD197714 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION molecule participating in vasculogenic response.
BD197714
VERSION BD197714.1 GI:33007484
KEYWORDS JP 2002509721-A/740.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P.A., Roberts, E., Jarvie, T., Coeshott, C. and Mcswiggen, J.A.
TITLE Method and reagent for treating diseases or conditions concerning
JOURNAL molecule participating in vasculogenic response
COMMENT Patent: JP 2002509721-A 740 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/740
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P23/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC

C12N5/00

CC Method and reagent for treating diseases or conditions CC

CC concerning molecule

CC participating in vasculogenic response

FH Key Location/Qualifiers

FT source 1..17

FT Location/Qualifiers /organism='Homo sapiens (human)'

source

1..17

/organism='Homo sapiens'

/mol_type='genomic RNA'

/db_xref='taxon:9606'

ORIGIN

Query Match

Best Local Similarity 67.8%; Score 12.2; DB 6; Length 17;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

1 CCCCCCTTCTGGATA 17

Db 1 CCCCCCTTCTGGATA 17

RESULT 15

112779

LOCUS Sequence 77 from patent US 5427930. 23 bp DNA linear PAT 26-JUL-1995

ACCESSION 112779

VERSION 112779.1 GI:910161

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 23)

AUTHORS Birkenmeyer,L.G., Carrino,J.J., Dille,B.J., Hu,H.-Y.,

Kratovich,J.D., Laffler,T.G., Marshall,R.L., Rinehardt,L.A. and

Solomon,N.A.

TITLE Amplification of target nucleic acids using gap filling ligase

JOURNAL Patent: US 5427930-A 77 27-JUN-1995;

FEATURES Location/Qualifiers

source 1..23

/organism='unknown'

/mol_type='unassigned DNA'

ORIGIN

Query Match

Best Local Similarity 67.8%; Score 12.2; DB 6; Length 23;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

2 CCCCCCTTCTGGATA 18

Db 1 CCCCCCTTCTGGATCC 17

Search completed: April 7, 2006, 14:36:14
Job time : 940.432 secs

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CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clones) and type
CC C (e.g., R3clone417). The invention also encompasses isolated 16S rRNA
CC gene sequences of the ammonia-oxidising bacteria of the invention,
CC oligonucleotide probes and primers for the detection of these bacteria,
CC and compositions comprising the bacteria. The bacteria of the invention
CC are useful in biological filters for reducing ammonia accumulation in
CC both freshwater and seawater aquaria. They may also be used in waste
CC water treatment and in bioremediation processes to reduce the level of
CC pollution caused by ammonia. The present sequence represents a
CC specifically claimed probe for the detection of the 16S rRNA gene
CC sequences of the type A and A1 ammonia-oxidising bacteria (ABA02416-
CC ABA02417). (updated on 29-AUG-2003 to standardise OS field)

CC Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTTCGATAC 18
1 CCCCCCTCTTCGATAC 18

RESULT 2

ADM32708
ID ADM32708 standard; DNA; 18 BP.

AC ADM32708;

DT 17-JUN-2004 (first entry)

XX Nitrosospira-like 16S rDNA probe. S-G-Nsapa-0149-a-a-18.

XX 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;

XX aqueous environment; freshwater; seawater; aquarium; ser. probe.

OS Nitrosospira sp.

PN MO2004026772-A2.

PD 01-APR-2004.

XX 10-SEP-2003; 2003WO-US028210.

PR 19-SEP-2002; 2002US-0386217P.

PR 19-SEP-2002; 2002US-0386218P.

PR 19-SEP-2002; 2002US-0386219P.

PA (AOQA-) AQUARIA INC.

PI Hovanec TA;

DR MPI; 2004-304936/28.

PT New composition comprising an isolated bacterial strain that oxidizes

PT ammonia to nitrite, useful for alleviating or preventing the accumulation

PT of ammonia in aqueous environment.

PS Example 6; Page 34; 98pp; English.

XX This sequence represents a probe which was used in the detection of 16S
CC rDNA sequence derived from an ammonia oxidising bacteria (AOB). The
CC amplified sequence may be used in a composition which comprises an
CC isolated bacterial strain that oxidizes ammonia to nitrite. The
CC composition may be used for alleviating or preventing the accumulation of
CC ammonia in a medium. The ammonia is reduced by at least 30% when compared
CC with a level of ammonia that would exist in the absence of the bacterial
CC strain. The composition is useful for alleviating or preventing the
CC accumulation of ammonia in aqueous environment, e.g. a freshwater or
CC seawater aquarium.

SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTTCGATAC 18
1 CCCCCCTCTTCGATAC 18

RESULT 3

ABT39927
ID ABT39927 standard; DNA; 17 BP.

AC ABT39927;

DT 13-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 5564.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;

XX antiense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

XX schizoprenia; protein chip; gene therapy; tumour suppression;

XX human fukutin; ds.

OS Homo sapiens.

PN MO2003025175-A2.

PD 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

PA Telerman A, Amson R, Tuijnder M;

DR MPI; 2003-31353/30.

PT New isolated nucleic acid, useful for treating viral diseases associated

PT with tumors and cell degeneration, also related polypeptides, antibodies

PT and transfected cells.

PS Disclosure; Page 684; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizoprenia. Analaysis of the expression and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

SQ Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCTGGATAC 18
 |||||
 DB 3 TCTTCTGGATAC 14

RESULT 4
 ACC67980
 ID ACC67980 standard; DNA; 17 BP.
 AC ACC67980;
 XX
 XX
 DT 01-JUL-2003 (first entry)
 XX
 XX Murine oligonucleotide associated with tumour suppression, SEQ ID 5227.
 XX
 KM Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; murine;
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;
 KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; ss.
 XX
 OS Mus musculus.
 OS
 PN WO2003025176-A2.
 XX
 XX
 PD 27-MAR-2003.
 XX
 XX 17-SEP-2002; 2002WO-1B004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 XX (MOLF-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 642; 738pp; French.
 XX
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC6806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterized by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 CC
 XX
 XX Sequence 17 BP; 1 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCCTCTTCTGG 14
 |||||
 DB 4 CCCCTCTTCTGG 15

RESULT 5
 ADB43132
 ID ADB43132 standard; DNA; 17 BP.
 AC ADB43132;
 XX
 XX

XX
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 XX Tumour suppression/reversion associated nucleotide #3455.
 DE
 XX
 KM Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KM primer; probe; tumour suppression; tumour reversion; apoptosis;
 KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KM diagnosis.
 XX
 OS Homo sapiens.
 OS
 PN WO2003040369-A2.
 XX
 XX
 PD 15-MAY-2003.
 XX
 XX 17-SEP-2002; 2002WO-1B004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 XX (MOLF-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-441574/41.
 XX
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 PS Disclosure; Page 435; 771pp; French.
 XX
 XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acid, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptides are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 XX Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCTGGATAC 18
 |||||
 DB 3 TCTTCTGGATAC 14

RESULT 6
 ADH30251
 ID ADH30251 standard; DNA; 17 BP.
 AC ADH30251;
 XX
 XX
 DT 11-MAR-2004 (first entry)
 XX

DE Human monocyte-macrophage cell surface apob48 receptor primer #5.
 XX antilipemic; gene therapy;
 KW monocyte-macrophage cell surface apob48 receptor; apob48R;
 KM pattern B phenotype; familial combined hyperlipidaemia;
 KW hypercholesterolaemia; hypertriglyceridaemia;
 KM low plasma high-density lipoprotein level; human; primer; ss.
 XX Homo sapiens.
 XX US2003208060-A1.
 PN 06-NOV-2003.
 PD 12-JUN-2003; 2003US-00459876.
 PF 06-AUG-1998; 98US-00130242.
 PR 31-MAY-2000; 2000US-00583610.
 XX (GIAN/) GIANTURCO S H.
 PA (BRAD/) BRADLEY W A.
 PI Gianturco SH, Bradley WA;
 DR WPI; 2003-864799/80.
 XX New isolated DNA molecule encoding a monocyte-macrophage cell surface
 PT apob48 receptor protein (apob48R), useful in preparing a composition for
 PT treating e.g., familial or non-familial hypercholesterolemia.
 XX Example 23; SEQ ID NO 17; 77pp; English.
 CC The invention describes a new isolated DNA molecule, encoding a monocyte-
 CC macrophage cell surface apob48 receptor protein (apob48R) comprising a
 CC fully defined 1088 amino acid sequence. The DNA molecule is useful in
 CC preparing a composition for treating Pattern B phenotype, familial
 CC combined hyperlipidaemia, familial or non-familial hypercholesterolemia,
 CC hypertriglyceridaemia or low plasma high-density lipoprotein levels. This
 CC sequence represents a primer used in the isolation of human monocyte-
 CC macrophage cell surface apob48 receptor DNA.
 XX Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 66.7%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCTCTCTGGAT 16
 DB 5 CCTCTCTGGAT 16
 RESULT 7
 ADO00840
 ID ADO00840 standard; DNA; 17 BP.
 XX ADO00840; Y
 AC 12-AUG-2004 (first entry)
 DT Human monocyte-macrophage cell surface apob48R cDNA PCR primer #6.
 XX
 DE Human monocyte-macrophage cell surface apolipoprotein B 48 receptor;
 KW apolipoprotein B 48 receptor; apob48R; PCR; ss; monocyte; macrophage;
 KW reticuloendothelial cell; monocyte adhesion; cardiovascular disease;
 KW apob-mediated cellular uptake; plasma chylomicron;
 KM hypertriglyceridaemia; triglyceride-rich lipoprotein;
 KM apob independent pathway; lipoprotein lipase independent pathway;
 KW heparin sulfate proteoglycan independent pathway; foam cell formation;
 KW hypertriglyceridaemia; primer.
 XX Homo sapiens.
 XX

PN US6740735-B1.
 XX 25-MAY-2004.
 PD 31-MAY-2000; 2000US-00583610.
 PF 06-AUG-1998; 98US-00130242.
 XX (GIAN/) GIANTURCO S H.
 PA (BRAD/) BRADLEY W A.
 PI Gianturco SH, Bradley WA;
 DR WPI; 2004-387250/36.
 PD New isolated monocyte-macrophage cell surface apob48 receptor protein,
 PT useful for cell-specific delivery of therapeutic compounds to human
 PT monocytes or macrophages, or for evaluating an individual at risk for
 PT cardiovascular disease.
 XX Example 23; SEQ ID NO 17; 72pp; English.
 CC The invention relates to the human monocyte-macrophage cell surface
 CC apolipoprotein B 48 receptor (apob48R) protein and the nucleic acid
 CC encoding it. The invention also relates to a method of cell-specific
 CC delivery of therapeutic compounds to human monocytes, macrophages or
 CC other reticuloendothelial cells that express the receptor, a method of
 CC inhibiting foam cell formation and increased monocyte adhesion to
 CC endothelial cells and a method of evaluating an individual at risk of a
 CC cardiovascular disease. The monocyte-macrophage cell surface apob48
 CC receptor protein is useful in the apob-mediated cellular uptake of plasma
 CC chylomicrons and remnants and hypertriglyceridaemic triglyceride-rich
 CC lipoproteins in an apob independent pathway, a lipoprotein lipase
 CC independent pathway or a heparin sulfate proteoglycan independent
 CC pathway. It is also useful for the cell-specific delivery of therapeutic
 CC compounds to human monocytes, macrophages or other reticuloendothelial
 CC cells that express the receptor, for inhibiting foam cell formation and
 CC increased monocyte adhesion to endothelial cells and for evaluating an
 CC individual at risk of a cardiovascular disease such as
 CC hypertriglyceridaemia. This sequence represents a PCR primer used in
 CC cloning of cDNA encoding the apob48R protein of the invention.
 XX Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 66.7%; Score 12; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCTCTCTGGAT 16
 DB 5 CCTCTCTGGAT 16
 RESULT 8
 ABA02421/c
 ID ABA02421 standard; DNA; 18 BP.
 XX ABA02421;
 AC 29-AUG-2003 (revised)
 DT 04-MAR-2002 (first entry)
 DE Type A/Al ammonia-oxidising bacterium 16S rRNA gene forward PCR primer.
 XX
 XX Type A; type Al; ammonia-oxidising bacterium; AOB; nitrite;
 KW 16S rRNA gene; ribosomal RNA; aquarium; aquaculture;
 KW waste water treatment; bioremediation; PCR primer; ss.
 XX Nitrosomonadales.
 OS
 XX WO200190312-A1.
 PN 29-NOV-2001.
 XX

```

XX PF 17-MAY-2001; 2001WO-US016265.
XX PR 19-MAY-2000; 2000US-00573684.
XX PA (AQUA-) AQUARIA INC.
XX PI Hovanec TA, Burrell PC;
XX WPI; 2002-075367/10.
XX DR
XX PT New bacteria capable of oxidizing ammonia to nitrite, for preventing or
XX PT alleviating the accumulation of ammonia in fresh water aquaria, seawater
XX PT aquaria and where water.
XX PS Example; Page 10; 62pp; English.
XX CC The invention relates to 4 novel types of ammonia-oxidizing bacteria
XX CC (AOB) found in freshwater aquaria. The bacteria are able to oxidize
XX CC ammonia to nitrite and are members of the ammonia-oxidizing bacteria
XX CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria
XX CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
XX CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
XX CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
XX CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
XX CC gene sequences of the ammonia-oxidizing bacteria of the invention,
XX CC oligonucleotide probes and primers for the detection of these bacteria,
XX CC and compositions comprising the bacteria. The bacteria of the invention
XX CC are useful in biological filters for reducing ammonia accumulation in
XX CC both freshwater and seawater aquaria. They may also be used in waste
XX CC water treatment and in bioremediation processes to reduce the level of
XX CC pollution caused by ammonia. Sequences ABA02421-ABA02422 represent PCR
XX CC primers for the detection of the 16S rRNA gene sequences of the type A
XX CC and A1 ammonia-oxidizing bacteria (ABA02416-ABA02417). (Updated on 29-AUG
XX CC -2003 to standardise OS field)
XX SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 6; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 7.5e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 TCTTCGTGATAC 18
XX DB 18 TCTTCGTGATAC 7
XX
XX RESULT 9
XX ADM32709/c
XX ID ADM32709 standard; DNA; 18 BP.
XX AC ADM32709;
XX DT 17-JUN-2004 (first entry)
XX DE Type A AOB 16S rDNA forward primer.
XX KW 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;
XX KW aqueous environment; freshwater; seawater; aquarium; ss; primer.
XX OS Nitrosomonas aestuarii.
XX PN WO2004026772-A2.
XX PD 01-APR-2004.
XX PF 10-SRP-2003; 2003WO-US028210.
XX PR 19-SRP-2002; 2002US-0386217P.
XX PR 19-SRP-2002; 2002US-0386218P.
XX PR 19-SRP-2002; 2002US-0386219P.
XX PA (AQUA-) AQUARIA INC.

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XX PI Hovanec TA;
XX DR WPI; 2004-304936/28.
XX PT New composition comprising an isolated bacterial strain that oxidizes
XX PT ammonia to nitrite, useful for alleviating or preventing the accumulation
XX PT of ammonia in aqueous environment.
XX PS Example 7; Page 34; 98pp; English.
XX CC This sequence represents a primer which was used in the detection of 16S
XX CC rRNA sequence derived from an ammonia oxidizing bacteria (AOB). The
XX CC amplified sequence may be used in a composition which comprises an
XX CC isolated bacterial strain that oxidizes ammonia to nitrite. The
XX CC composition may be used for alleviating or preventing the accumulation of
XX CC ammonia in a medium. The ammonia is reduced by at least 30% when compared
XX CC with a level of ammonia that would exist in the absence of the bacterial
XX CC strain. The composition is useful for alleviating or preventing the
XX CC accumulation of ammonia in aqueous environment, e.g. a freshwater or
XX CC seawater aquarium.
XX SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 12; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 7.5e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 TCTTCGTGATAC 18
XX DB 18 TCTTCGTGATAC 7
XX
XX RESULT 10
XX AAF6277/c
XX ID AAF6277 standard; DNA; 19 BP.
XX AC AAF6277;
XX DT 24-JUL-2001 (first entry)
XX DE Mutated cPPT fragment cPPT-225 SEQ ID 23.
XX KW Triplex; cis-polyurine tract; cPPT; central termination sequence; CTS;
XX KW cis acting region; retrovirus; blood disorder; developmental disorder;
XX KW brain disorder; nervous system disorder; ss.
XX OS Human immunodeficiency virus 1.
XX OS Synthetic.
XX PN WO200127304-A2.
XX PD 19-APR-2001.
XX PF 10-OCT-2000; 2000WO-EP010418.
XX PR 12-OCT-1999; 99US-0158387P.
XX PA (INSP ) INST PASTEUR.
XX PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX PI Charneau P, Zennou V, Pflumio F, Silven A, Dubart Kupperschmitt A;
XX DR WPI; 2001-273782/28.
XX PT New nucleic acid, useful for prophylactic, ameliorative or curative
XX PT treatment of genetic diseases, comprises retroviral cis-polyurine tract
XX PT and central termination sequence cis acting regions.
XX PS Example 2; Fig 1A; 81pp; English.
XX CC This invention relates to a triple stranded nucleic acid structure
XX CC containing at least one copy of the cis-polyurine tract (cPPT) and

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CC central termination sequence (CTS) cis acting regions of a retrovirus.
CC The cPPT region initiates synthesis of a downstream plus strand during
CC reverse transcription and CTS is involved in the termination and ejection
CC of reverse transcriptase. The cPPT and CTS regions induce a 3-stranded
CC DNA structure which stimulates entry of nucleic acids into the nucleus of
CC cells. The triple structures can act as nucleic acid importers into non-
CC dividing target cells. The nucleic acid, and vectors containing it are
CC useful for the prophylactic, ameliorative or curative treatment of an
CC individual suffering from or having a high likelihood of developing a
CC disease or disorder with a genetic basis. Therapeutic proteins can be
CC administered to a patient using a vector containing DNA encoding the
CC protein and the nucleotide sequence of the invention. Diseases and
CC disorders which can be treated include blood disorders, brain or nervous
CC system disorders or developmental disorders. The present sequence
CC represents a mutated fragment of the HIV-1 cPPT sequence. Wild type cPPT
CC and various mutant versions of cPPT are used in an example illustrating
CC that central initiation of reverse transcription is an essential step of
CC the HIV-1 replicative cycle

XX SQ Sequence 19 BP; 7 A; 0 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCCCTCTTCT 12
DB 19 CCCCCCTCTTCT 8

RESULT 11
ADE10102/c
ID ADE10102 standard; DNA; 19 BP.

XX ADE10102;

DT 29-JAN-2004 (first entry)

DE DNA encoding HIV-1 cPPT mutant (cPPT-AG) peptide.

XX Lentivirus; HIV-1; polypurine tract cis-active; cPPT;

KM central termination sequence; CTS; three-stranded DNA;

KM triplex DNA structure.; gene therapy; brain disease;

XX developmental disease; neuroprotective; gene therapy; mutant; ds.

XX Synthetic.

OS Human immunodeficiency virus 1.

XX Key

PH CDS

FT 1.19

FT /tag= a

FT /partial

FT /note= "This sequence lacks both start and stop codons"

FT /transl_except= (pos:1,aa:asn)

FT /note= "This codon has an apparent 2 nucleotide deletion

XX which alters the reading frame"

XX US2003194392-A1.

XX 16-OCT-2003.

XX 10-APR-2002; 2002US-00122114.

XX 10-APR-2002; 2002US-00122114.

XX (CHAR/) CHARNEAU P.

XX (ZENN/) ZENNOU V.

XX (PFLU/) PFLUMIO F.

XX (SIRV/) SIRVEN A.

XX (KUPP/) DUBART KUPPERSCHMITT A.

XX Charneau P, Zenou V, Pflumio F, Sirven A, Dubart Kupperschmitt A;

DR WPI; 2003-844442/78.

XX P-PSDB; ADE10101.

XX New nucleic acid comprising at least one copy of the cPPT and CTS cis-

PT acting regions of a retrovirus that induce a three-stranded DNA

PT structure, useful for preparing a composition for treating e.g., brain or

PT developmental disease.

XX Example 2; Fig 1A; 42bp; English.

XX The present invention relates to the isolation of a lentiviral

CC polynucleotide (e.g. HIV-1) polypurine tract cis-active (cPPT) and

CC central termination sequence (CTS) cis-acting regions that induce a three

CC stranded or triplex DNA structure. The lentiviral polynucleotide

CC sequences are useful in gene therapy for preparing a composition for

CC treating an individual suffering from, or having a likelihood of

CC developing a disorder such as brain or developmental disease. The present

CC sequence encodes a mutant HIV-1 cPPT peptide.

XX SQ Sequence 19 BP; 7 A; 0 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCCCTCTTCT 12
DB 19 CCCCCCTCTTCT 8

RESULT 12
AA14630/c
ID AA14630 standard; DNA; 20 BP.

XX AA14630;

DT 24-MAR-1999 (first entry)

DE Triple helix forming nucleotides 2407-2426 of the n-myc gene.

XX Triple-helix forming region; Triplex formation; DNA detection;

KM identification; bacteria; oncogene; virus; ds.

XX Homo sapiens.

OS US5861244-A.

XX 19-JAN-1999.

XX 22-DEC-1993; 93US-00173489.

XX 29-OCT-1992; 92US-00968436.

XX (PROF-) PROFILE DIAGNOSTIC SCI INC.

XX Hepburn AG, Wang C;

XX WPI; 1999-130384/11.

XX Assay of genetic sequences based on triplex formation from double

PT stranded analyte - and hybrid of anchor and reporter sequences, with

PT reporter released if triplex formation occurs, used e.g. to identify

PT bacteria.

XX Disclosure; Col 13-14; 168bp; English.

XX The present sequence represents a potential triple-helix forming region.

CC It can be used to demonstrate the assay of the invention. The assay

CC comprises adding a sample containing double-stranded DNA test sequences,

CC e.g. containing the present sequence, to an aqueous medium containing at

CC least one complex of anchor DNA, attached to a solid support, and

CC reporter DNA, where either a part of the anchor DNA or reporter DNA is

CC designed to form a triple-strand structure with part of the test

CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
SQ Sequence 20 BP; 7 A; 0 C; 13 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCT 12
DB 18 CCCCCCTCTCT 7

RESULT 13
AAX93192
ID AAX93192 standard; DNA; 20 BP.

AC AAX93192;

DT 13-SBP-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.

OS Synthetic.

OS Chlamydia pneumoniae.

PN WO927105-A2.

PD 03-JUN-1999.

PF 20-NOV-1998; 98WO-1B001890.

PR 21-NOV-1997; 97FR-00014673.

PR 04-NOV-1998; 98US-0107078P.

PA (GSEST) GENSEFT.

XX Griffais R;

DR WPI; 1999-357842/30.

PT Genome sequence of Chlamydia pneumoniae.

PS Page 1570; Disclosure; 1912pp; English.

CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae

XX Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGGAT 16
DB 11 CCCCCCTCTCT 7

DB 4 CCTCTTCTGGAT 15

RESULT 14
ID AAS97903/c
AAS97903 standard; DNA; 20 BP.

AC AAS97903;

DT 12-MAR-2002 (first entry)

DE Murine SACL gene-specific oligonucleotide PCR primer #456.

KW Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;
KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KW protein replacement therapy.

XX Mus sp.

PN WO200183749-A2.

PD 08-NOV-2001.

PF 25-APR-2001; 2001WO-US013387.

PR 28-APR-2000; 2000US-0200794P.

PR 28-JUL-2000; 2000US-0221419P.

PR 10-NOV-2000; 2000US-0247443P.

PA (WARN) WARNER LAMBERT CO.

PI (MONTE-) MONTELL CHEM SENSES CENT.

PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
PI Ohmen JD, Reed DR, Ross D, Tordoff MG;

DR WPI; 2002-075162/10.

PT Novel isolated polypeptide comprising variant form of mouse or human SACL
PT polypeptide, and is associated with altered preference for carbohydrates
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

PS Claim 14; Page 92; 239pp; English.

CC The invention relates to an isolated polypeptide, comprising a variant
CC form of mouse or human SACL polypeptide. The variant form is associated
CC with altered preference for carbohydrates, other sweeteners or ethanol.
CC The polypeptide and its associated DNA sequence can be produced by
CC recombinant techniques and is useful for preventing obesity, diabetes or
CC alcoholism associated with SACL expression. The sequences are useful in
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
CC embryos may be used in screening for and identifying agents that induce
CC or repress function of SACL. Predilection to diabetes, obesity or
CC alcoholism can be ascertained by testing any fluid or tissue of a human
CC (such as blood, pancreas or tongue) for sequence variations of the SACL
CC gene. A sequence variation of the SACL locus may indicate a
CC predisposition to diabetes, obesity and/or alcoholism and may provide a
CC diagnostic mark. The polynucleotide can be detected in a biological
CC sample by contacting the DNA with a probe to form a hybridisation complex
CC which is then detected. The sequences represent cDNA encoding human and
CC mouse SACL polypeptides and PCR primers specific for the SACL genes

XX Sequence 20 BP; 7 A; 6 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCTTCTGGA 15
DB 19 CCTCTTCTGGA 8

```

RESULT 15
ID ABX13323/c
XX ABX13323 standard; DNA; 20 BP.
XX
AC ABX13323;
XX
DT 14-MAY-2003 (first entry)
XX
DE Human NSDHL gene, exon 8 PCR primer #4.
XX
XX Human; ss; PCR; 3beta-hydroxysteroid dehydrogenase; 3beta-HSD; NSDHL;
KM cholesterol biosynthesis; mevalonic aciduria; desmosterolosis;
KM Smith-Lemli-Opitz syndrome; SLOS; Conradi-Hunermann-Happle syndrome;
KM chondroplasia punctata; X-linked disease; chromosome Xq28; psoriasis;
KM CHILD syndrome; bone disorder; osteoporosis; osteosclerosis;
KM congenital hemidysplasia; ichthyosiform erythroderma and limb defect;
KM ichthyosis; eye disorder; cataract; microphthalmia; arthritis;
KM cholest-8(9)-en-3beta-ol; skin disorder; primer.
XX
XX Homo sapiens.
OS
XX US2002172956-A1.
XX
XX 21-NOV-2002.
XX
XX 05-SEP-2001; 2001US-00946406.
XX
XX 01-JUN-1999; 99US-0137020P.
XX
XX 01-JUN-2000; 2000US-00588976.
XX
XX (CHIL-) CHILDRENS HOSPITAL INC.
XX
XX Herman GE, Kelley RI, Grange DK;
XX
XX WPI; 2003-310984/30.
XX
XX
XX Diagnosing CHILD syndrome or psoriasis, by detecting differences between
PT patient and wild type genes encoding 3 beta-hydroxysteroid dehydrogenase
PT or accumulation of sterol intermediates in body fluids of the patient.
XX
XX
XX Disclosure; Page 2; 23pp; English.
XX
XX
XX The invention relates to diagnosing congenital hemidysplasia,
XX ichthyosiform erythroderma and limb defects (CHILD) syndrome or psoriasis
XX in a patient, involves detecting nucleotide difference between patient
XX NSDHL oligonucleotide (gene encoding 3beta-hydroxysteroid dehydrogenase
XX (3beta-HSD)) and wild type NSDHL gene, or detecting accumulation of
XX sterol intermediates before the generation of cholest-8(9)-en-3beta-ol in
XX the cholesterol biosynthetic pathway, in the body fluids or cells of the
XX patient. The method is useful for diagnosing CHILD syndrome and psoriasis
XX in a patient. Other diseases implicated in defects of the cholesterol
XX biosynthetic pathway include mevalonic aciduria, desmosterolosis, Smith-
XX Lemli-Opitz syndrome (SLOS), Conradi-Hunermann-Happle syndrome;
XX chondroplasia punctata (X-linked disease), bone disorders, osteoporosis,
XX osteosclerosis, skin disorders, ichthyosis, eye disorders, cataracts,
XX and microphthalmia and arthritis. The human NSDHL gene is located on
XX chromosome X128. The present sequence is a primer for routine sequencing
XX of and mutation detection in the human NSDHL gene (one of 8 exons or the
XX non-coding region)
XX
XX
XX Sequence 20 BP; 8 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 66.7%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCCCTCTTCGG 14
DB 20 CCCCTCTTCGG 9

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:39:24 ; Search time 105.566 Seconds

(without alignments)
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Gapop 60.0, Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

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Total number of hits satisfying chosen parameters: 1026028

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	66.7	17	US-09-583-610D-17	Sequence 17, Appl
2	12	66.7	20	US-08-173-489C-17	Sequence 17, Appl
3	12	66.7	20	US-09-198-452A-2493	Sequence 2493, Ap
4	12	66.7	20	US-10-002-623-451	Sequence 451, App
5	12	66.7	25	US-09-396-196G-24325	Sequence 24325, A
6	11	61.1	15	US-09-094-714A-4	Sequence 4, Appl
7	11	61.1	18	US-09-474-922A-14	Sequence 14, Appl
8	11	61.1	20	US-09-280-799-154	Sequence 154, Appl
9	11	61.1	20	US-09-277-020-18	Sequence 18, Appl
10	11	61.1	20	US-09-060-299-126	Sequence 126, App
11	11	61.1	22	US-09-402-923A-126	Sequence 126, App
12	11	61.1	22	US-08-117-952-432	Sequence 432, App
13	11	61.1	25	US-10-341-199-18	Sequence 18, Appl
14	11	61.1	25	US-08-538-875-24	Sequence 24, Appl
15	11	61.1	25	US-09-142-355B-23	Sequence 23, Appl
16	11	61.1	25	US-09-699-931-23	Sequence 23, Appl
17	11	61.1	25	US-09-396-196G-10385	Sequence 10385, A
18	11	61.1	25	US-09-396-196G-10387	Sequence 10387, A
19	11	61.1	25	US-09-396-196G-10388	Sequence 10388, A
20	11	61.1	25	US-09-396-196G-10388	Sequence 10388, A
21	11	61.1	25	US-09-396-196G-19355	Sequence 19355, A
22	11	61.1	25	US-09-396-196G-37093	Sequence 37093, A
23	11	61.1	25	US-09-396-196G-37094	Sequence 37094, A
24	11	61.1	25	US-09-396-196G-52013	Sequence 52013, A

25	11	61.1	25	3	US-09-396-196G-52014	Sequence 52014, A
26	11	61.1	25	3	US-09-396-196G-52015	Sequence 52015, A
27	11	61.1	25	3	US-09-396-196G-52016	Sequence 52016, A
28	11	61.1	25	3	US-09-396-196G-52017	Sequence 52017, A
29	11	61.1	25	3	US-09-396-196G-52911	Sequence 52911, A
30	11	61.1	25	3	US-09-396-196G-62035	Sequence 62035, A
31	11	61.1	25	3	US-09-396-196G-66069	Sequence 66069, A
32	11	61.1	25	3	US-09-396-196G-84553	Sequence 84553, A
33	11	61.1	25	3	US-09-396-196G-84554	Sequence 84554, A
34	11	61.1	25	3	US-09-396-196G-84565	Sequence 84565, A
35	11	61.1	25	3	US-09-396-196G-86459	Sequence 86459, A
36	11	61.1	25	3	US-09-396-196G-100179	Sequence 100179, A
37	11	61.1	25	3	US-09-396-196G-100180	Sequence 100180, A
38	11	61.1	25	3	US-09-396-196G-103140	Sequence 103140, A
39	11	61.1	25	3	US-09-396-196G-103141	Sequence 103141, A
40	11	61.1	25	3	US-09-396-196G-117806	Sequence 117806, A
41	11	61.1	28	2	US-08-579-777A-4	Sequence 4, Appl
42	10	55.6	15	2	US-08-311-486C-125	Sequence 125, App
43	10	55.6	15	2	US-08-311-486C-126	Sequence 126, App
44	10	55.6	15	2	US-08-311-486C-127	Sequence 127, App
45	10	55.6	15	3	US-08-929-856-58	Sequence 58, Appl

ALIGNMENTS

```
RESULT 1
US-09-583-610D-17
Sequence 17, Application US/09583610D
Patent No. 6740735
GENERAL INFORMATION:
APPLICANT: Gianturco, S.H.
APPLICANT: Bradley, W.A.
TITLE OF INVENTION: DNA Encoding Human apob48R: A Monocyte-Macrophage
FILE REFERENCE: D5880CIP
CURRENT APPLICATION NUMBER: US/09/583, 610D
CURRENT FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 09/130,242
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 17
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Antisense primers were based on the 5'-end
of the THP-1 (73 clone (bp 2203-2187
US-09-583-610D-17
Query Match 66.7%; Score 12; DB 3; Length 17;
Best local Similarity 100.0%; Pred. No. 1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 5 CCTCTTCTGGAT 16
Db 5 CCTCTTCTGGAT 16
RESULT 2
US-08-173-489C-17/c
Sequence 17, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: MANG, C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
```

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; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelsman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: US9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION: n-myc gene (Accession # Y00664)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Ibsen, J M, Rabbits, P H.
; TITLE: Sequence of a germ-line N-myc
; Patent No. 5861244
; TITLE: Gene and amplification as a mechanism of
; TITLE: activation
; JOURNAL: Oncogene
; VOLUME: 2
; PAGES: 399-402
; DATE: 1988
; RELEVANT RESIDUES IN SEQ ID NO: 17 :FROM 1 TO 20
US-08-173-489C-17

Query Match          66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCCCCTCTCT 12
        |||||
Db      18 CCCCCCTCTCT 7

RESULT 3
US-09-198-452A-2493
; Sequence 2493, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2493
; LENGTH: 20
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```

; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-2493

Query Match          66.7%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCTCTCTCGAT 16
        |||||
Db      4 CCTCTCTCGAT 15

RESULT 4
US-10-002-623-451
; Sequence 451, Application US/10002623
; Patent No. 6929911
; GENERAL INFORMATION:
; APPLICANT: OEFNER, PETER J.
; APPLICANT: UNDERHILL, PETER A.
; TITLE OF INVENTION: A METHOD FOR DETERMINING GENETIC
; TITLE OF INVENTION: AFFILIATION, SUBSTRUCTURE AND GENE FLOW WITHIN HUMAN
; FILE REFERENCE: STAN-212
; CURRENT APPLICATION NUMBER: US/10/002,623
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/245,355
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 952
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 451
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-002-623-451

Query Match          66.7%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CCCCCCTCTCTG 13
        |||||
Db      9 CCCCCCTCTCTG 20

RESULT 5
US-09-396-196G-24325
; Sequence 24325, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24325
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24325

Query Match          66.7%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CCTCTCTCTGGA 15
```


Db 3 CCCCTCTCTGGA 14

RESULT 6
US-09-094-714A-4
Sequence 4, Application US/09094714A
Patent No. 6117847

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Nicholas M. Dean

TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF

TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 611784719, LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 1. DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/094,714A

FILING DATE: June 15, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,269

FILING DATE: 14-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/478,178

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/089,996

FILING DATE: 09-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/852,852

FILING DATE: 16-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legaard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: ISIS-2943

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 15

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-094-714A-4

Query Match 61.1%; Score 11; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCCTCTCTCT 12

Db 2 CCCCTCTCTCT 12

RESULT 7

US-09-474-922A-14

Sequence 14, Application US/09474922A

Patent No. 6187586

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Lex M. Cowsett

APPLICANT: Richard A. Roth

TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION

FILE REFERENCE: RTS-0036

CURRENT APPLICATION NUMBER: US/09/474,922A

CURRENT FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 14

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-474-922A-14

Query Match 61.1%; Score 11; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCCTCTCTG 13

Db 2 CCCCTCTCTG 12

RESULT 8

US-09-280-799-154

Sequence 154, Application US/09280799

Patent No. 6136603

GENERAL INFORMATION:

APPLICANT: Dean, Nicholas M.

APPLICANT: Karrera, James G

APPLICANT: McKay, Robert

TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL

TITLE OF INVENTION: TRANSDUCTION

FILE REFERENCE: ISPH-0340

CURRENT APPLICATION NUMBER: US/09/280,799

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 154

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-280-799-154

Query Match 61.1%; Score 11; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.8e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCCCTCTCTG 14

Db 10 CCCCTCTCTG 20

RESULT 9

US-09-277-020-18

Sequence 18, Application US/09277020

Patent No. 6210892

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation

FILE REFERENCE: ISPH-0339

CURRENT APPLICATION NUMBER: US/09/277,020

CURRENT FILING DATE: 1999-03-26

EARLIER APPLICATION NUMBER: 09/167,921

EARLIER FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 18

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-277-020-18

Query Match 61.1%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCTTTGG 14
|||||
Db 10 CCTCTTTGG 20

RESULT 10
US-09-060-299-126
Sequence 126, Application US/09060299
Patent No. 6545137
GENERAL INFORMATION:
APPLICANT: Todd, John A
APPLICANT: Hees, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly
APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Metzger, Tony R
APPLICANT: Merriman, Michael L
TITLE OF INVENTION: No. 6545137el Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,299
FILING DATE: 15-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA: US 60/048,740
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-060-299-126

Query Match 61.1%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGA 15
|||||
Db 8 CCTCTTCTGA 18

RESULT 11
US-09-402-923A-126
Sequence 126, Application US/09402923A
Patent No. 6555654

GENERAL INFORMATION:
APPLICANT: Todd, John A
APPLICANT: Hees, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly
APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Metzger, Tony R
APPLICANT: Merriman, Michael L

TITLE OF INVENTION: No. 6555654el LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: VA 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-09-402-923A-126

Query Match 61.1%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGA 15
|||||
Db 8 CCTCTTCTGA 18

RESULT 12
US-08-117-952-432/c
Sequence 432, Application US/08117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.

```

; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Jipretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen B.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 432:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-432

Query Match      61.1%; Score 11; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY      5 CCTCTTCTGGA 15
DB      14 CCTCTTCTGGA 4

RESULT 13
US-10-341-199-18/c
; Sequence 18, Application US/10341199
; Patent No. 6852494
; GENERAL INFORMATION:
; APPLICANT: Liao, Haisun
; APPLICANT: Deik, Amy Anderson
; APPLICANT: Mamaeva, Natalia
; APPLICANT: Woodward, Caroline Ngaara
; APPLICANT: Chen, Shin-Yih
; APPLICANT: Huang, Yih
; APPLICANT: Shen, Ming
; APPLICANT: Law, Simon W.
; APPLICANT: Huang, Tai-Nang
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: 12251-036001
; CURRENT APPLICATION NUMBER: US/10/341,199
; CURRENT FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
; US-10-341-199-18

Query Match      61.1%; Score 11; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY      2 CCCCCCTTCTCT 12
DB      11 CCCCCCTTCTCT 1

RESULT 14
US-08-538-875-24/c
; Sequence 24, Application US/08538875
; Patent No. 5773582
; GENERAL INFORMATION:
; APPLICANT: Shin, Hang-Cheol
; APPLICANT: Shin, Nam-Kyu
; APPLICANT: Lee, Inkyung
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR MUTAINS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Shin, Hang-Cheol
; STREET: Jukong Gocheung Apt. 1014-806, Haan-dong
; CITY: Kwangmyung-shi
; STATE: Kyungki-do
; COUNTRY: Republic of Korea
; ZIP: 423-060
; ADDRESSEE: Shin, Nam-Kyu
; STREET: #181-404 Sadang-4-dong, Dongjak-ku
; CITY: Seoul
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 156-094
; ADDRESSEE: Lee, Inkyung
; STREET: 11/2, #302-39 Jnan-4-dong, Nam-ku
; CITY: Incheon
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 402-204
; ADDRESSEE: Kang, Sungzong
; STREET: #84-4 Daeshin-dong, Seodaemun-ku
; CITY: Seoul
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 120-160
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5inch 2.0Mb storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Nordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,336
; FILING DATE:
; APPLICATION NUMBER: KR 93-1751
; FILING DATE: 9-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 bases
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```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer DNA
US-08-538-875-24

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; Patent No. 6184012
; GENERAL INFORMATION:
; APPLICANT: Neri, Dario
; APPLICANT: Demartis, Salvatore
; APPLICANT: Huber, Adrain
; APPLICANT: Viti, Francesca
; APPLICANT: Tawfik, Dan. S.
; APPLICANT: Winter, Gregory, Paul
; TITLE OF INVENTION: Isolation of Enzymes
; FILE REFERENCE: 2224/08665
; CURRENT APPLICATION NUMBER: US/09/142,355B
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: GB 9608540.2
; PRIOR FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/GB97/01153
; PRIOR FILING DATE: 1997-04-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
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; LENGTH: 25
; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: primer
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ALIGNMENTS

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ORGANISM synthetic construct
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REFERENCE
1 Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 5 02-FEB-2005;
Aquadria Inc. (US)

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LOCUS
DEFINITION Sequence 5 from Patent WO0190312.
ACCESSION AX316096
VERSION AX316096.1 GI:17899287

KEYWORDS
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ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Hovanec, T.A. and Burrell, P.C.
AUTHORS Ammonia-oxidizing bacteria
TITLE Patent: WO 0190312-A 5 29-NOV-2001;
JOURNAL AQUARIA, INC. (US)

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RESULT 4
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LOCUS
DEFINITION Sequence 18 from Patent EP1502948.
ACCESSION CS089171
VERSION CS089171.1 GI:66714455

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Hovanec, T.A. and Burrell, P.C.
AUTHORS Ammonia-oxidizing bacteria
TITLE Patent: EP 1502948-A 18 02-FEB-2005;
JOURNAL Aquadia Inc. (US)

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RESULT 5
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LOCUS
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ACCESSION AX316109
VERSION AX316109.1 GI:17899300

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Hovanec, T.A. and Burrell, P.C.
AUTHORS Ammonia-oxidizing bacteria
TITLE Patent: WO 0190312-A 18 29-NOV-2001;
JOURNAL AQUARIA, INC. (US)

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AR568743 17 bp DNA linear PAT 14-DEC-2004

LOCUS
DEFINITION Sequence 17 from patent US 6740735.
ACCESSION AR568743
VERSION AR568743.1 GI:56568296

KEYWORDS
SOURCE unknown.
ORGANISM unknown.
unclassified.

REFERENCE
1 (bases 1 to 17)
AUTHORS Gianturco, S.H. and Bradley, W.A.
TITLE DNA encoding human apob48r: a monocyte-macrophage apolipoprotein
B48 receptor gene and protein
JOURNAL Patent: US 6740735-A 17 25-MAY-2004;
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ACCESSION AX727540
VERSION AX727540.1 GI:30506883
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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REFERENCE
AUTHORS Teleman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 5227 27-MAR-2003;
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ACCESSION AX733930
VERSION AX733930.1 GI:30513273
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
AUTHORS Teleman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 5564 27-MAR-2003;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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ACCESSION AX760134
VERSION AX760134.1 GI:32254750
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Teleman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 3455 15-MAY-2003;
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Molecular Engines Laboratories (FR)
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Db 3

RESULT 10
LOCUS CQ796913/C 18 bp DNA linear PAT 19-APR-2004
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ACCESSION CQ796913
VERSION CQ796913.1 GI:46408539
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Hovanec, T. A.
TITLE Ammonia-oxidizing bacteria and methods of using and detecting
JOURNAL Patent: WO 2004026772-A 6 01-APR-2004;
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RESULT 11
LOCUS CS089159/C 18 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 6 from Patent EP1502948.

```

ACCESSION   CS089159
VERSION     CS089159.1
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Hovanec, T.A. and Burrell, P.C.
  TITLE     Ammonia-oxidizing bacteria
  JOURNAL   Patent: EP 1502948-A 6 02-FEB-2005;
            Aquaria Inc. (US)
FEATURES    source
            1..18
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Description of Artificial Sequence: Primer"
ORIGIN
Query Match      66.7%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCTTCGTGATAC 18
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Db 18 TCTTCGTGATAC 7

RESULT 12
AX116097/c    18 bp    DNA    linear    PAT 14-DEC-2001
LOCUS         AX116097
DEFINITION    Sequence 6 from Patent WO0190312.
ACCESSION     AX116097
VERSION       AX116097.1
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
  AUTHORS     Hovanec, T.A. and Burrell, P.C.
  TITLE       Ammonia-oxidizing bacteria
  JOURNAL     Patent: WO 0190312-A 6 29-NOV-2001;
            AQUARIA, INC. (US)
FEATURES      location/Qualifiers
            1..18
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Primer"
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Query Match      66.7%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCTTCGTGATAC 18
    |||||
Db 18 TCTTCGTGATAC 7

RESULT 13
HSR2P011      18 bp    DNA    linear    PRI 13-DEC-1994
LOCUS         HSR2P011
DEFINITION    H.sapiens Ret Proto-Oncogene, Intron 11 (3').
ACCESSION     X79751
VERSION       X79751.1
KEYWORDS      Intron; ret gene; ret proto-oncogene.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE     1

```

```

AUTHORS       Mulligan, L.M., Eng, C., Attie, T., Lyonnet, S., Marsh, D.J.,
            Hyland, V.J., Robinson, B.G., Fritling, A., Verellen-Dumoulin, C.,
            Safar, A., Venter, D.J., Munich, A., and Ponder, B.A.J.
TITLE         Diverse phenotypes associated with exon 10 mutations of the RET
JOURNAL       Hum. Mol. Genet. 3 (12), 2163-2167 (1994)
PUBMED       7881414
REFERENCE     2 (bases 1 to 18)
AUTHORS       Eng, C.
TITLE         Direct Submission
JOURNAL       Submitted (14-JUN-1994) C. Eng, University of Cambridge, Dept of
            Pathology, Tennis Court Road, Cambridge CB2 1QP, UK
FEATURES      source
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              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /isolate="CB3"
              /db_xref="taxon:9606"
              /chromosome="10"
              /map="q11.2"
              /genome="Homo sapiens"
              /gene="RET"
              /number="11"
            intron
            1..18
              /gene="RET"
              /number="3" end"
ORIGIN
Query Match      66.7%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTCT 12
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Db 6 CCCCCCTCTTCT 17

RESULT 14
AX112294/c    19 bp    DNA    linear    PAT 01-MAY-2001
LOCUS         AX112294
DEFINITION    Sequence 23 from Patent WO0127304.
ACCESSION     AX112294
VERSION       AX112294.1
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
  AUTHORS     Charneau, P., Zennou, V., Pflumio, F., Silven, A. and Dubart
            Kupperchmidt, A.
  TITLE       Lentiviral triplex dna, and vectors and recombinant cells
            containing lentiviral triplex dna
  JOURNAL     Patent: WO 0127304-A 23 19-APR-2001;
            INSTITUT PASTEUR (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA
            RECHERCHE MEDICALE (INSERM) (FR)
FEATURES      location/Qualifiers
            1..19
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="MUTATION INTRODUCED INTO THE HIV-1 cPPT CODING
            SEQUENCE"
ORIGIN
Query Match      66.7%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTTCT 12
    |||||
Db 19 CCCCCCTCTTCT 8

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RESULT 15

AR029828/c

LOCUS

AR029828

20 bp

DNA

linear

PAT 29-SEP-1999

DEFINITION

Sequence 17 from patent US 5861244.

ACCESSION

AR029828

VERSION

AR029828.1 GI:5943042

KEYWORDS

UNKNOWN.

SOURCE

UNKNOWN.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Wang, C.-G. and Hepburn, A.G.

TITLE

Genetic sequence assay using DNA triple strand formation

JOURNAL

Patent: US 5861244-A 17 19-JAN-1999;

FEATURES

Location/Qualifiers

ORIGIN

1..20 /organism="unknown" /mol_type="unassigned DNA"

Query Match

66.7%; Score 12; DB 6; Length 20;

Best Local Similarity

100.0%; Pred. No. 2.9e+04;

Matches 12; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CCCCCCTCTCT 12

DB

18 CCCCCCTCTCT 7

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Job time : 925.838 secs

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:38:29 ; Search time 780.324 Seconds

(without alignments)
92.282 Million cell updates/sec

Title: US-10-659-980a-5

Perfect score: 18

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

13050014

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	14	77.8	25	US-10-310-914A-1061199
2	14	77.8	25	US-11-121-849-112898
3	13.8	76.7	19	US-11-101-244-1578545
4	13.8	76.7	19	US-11-083-784-1578545
5	13.8	76.7	25	US-11-121-849-325988
6	13.8	76.7	25	US-11-136-527-352597
7	13.8	76.7	25	US-11-136-527-352597
8	13.8	76.7	25	US-11-136-527-352597
9	13.4	74.4	21	US-10-310-914A-908031
10	13.4	74.4	24	US-10-310-914A-84927
11	13.4	74.4	25	US-11-121-849-394245
12	13.2	73.3	19	US-10-310-914A-1353078
13	13.2	73.3	19	US-11-101-244-1473850
14	13.2	73.3	19	US-11-083-784-1473850
15	13.2	73.3	21	US-10-770-726-11899
16	13.2	73.3	21	US-10-310-914A-896978
17	13.2	73.3	22	US-10-310-914A-691838
18	13.2	73.3	22	US-10-310-914A-691951

C	19	13.2	73.3	24	8	US-10-310-914A-447953	Sequence 447953,
	20	13.2	73.3	25	8	US-10-310-914A-935287	Sequence 935287,
	21	13.2	73.3	25	8	US-10-310-914A-967300	Sequence 967300,
	22	13.2	73.3	25	9	US-10-933-982-9664	Sequence 9664, Ap
	23	13.2	73.3	25	14	US-11-121-849-36513	Sequence 36513, A
	24	13.2	73.3	25	14	US-11-121-849-171065	Sequence 171065,
	25	13.2	73.3	25	14	US-11-121-849-377842	Sequence 377842,
	26	13.2	73.3	30	14	US-11-170-751-2	Sequence 2,
	27	13	72.2	19	12	US-11-101-744-1230837	Sequence 1230837,
	28	13	72.2	19	13	US-11-083-784-1230837	Sequence 1230837,
	29	13	72.2	23	8	US-10-310-914A-224598	Sequence 224598,
	30	13	72.2	25	9	US-10-934-048A-68320	Sequence 68320, A
	31	13	72.2	27	8	US-10-310-914A-224598	Sequence 224598,
	32	12.8	71.1	18	8	US-10-310-914A-896977	Sequence 896977,
	33	12.8	71.1	20	14	US-11-111-288-234	Sequence 234, App
	34	12.8	71.1	21	8	US-10-310-914A-447881	Sequence 447881,
	35	12.8	71.1	21	8	US-10-310-914A-1261081	Sequence 1261081,
	36	12.8	71.1	22	8	US-10-310-914A-466300	Sequence 466300,
	37	12.8	71.1	22	8	US-10-310-914A-899298	Sequence 899298,
	38	12.8	71.1	22	8	US-10-310-914A-1261104	Sequence 1261104,
	39	12.8	71.1	23	8	US-10-310-914A-764601	Sequence 764601,
	40	12.8	71.1	23	8	US-10-310-914A-830964	Sequence 830964,
	41	12.8	71.1	23	8	US-10-310-914A-1109455	Sequence 1109455,
	42	12.8	71.1	25	9	US-10-310-914A-1109461	Sequence 1109461,
	43	12.8	71.1	25	9	US-10-932-182A-70617	Sequence 70617, A
	44	12.8	71.1	25	9	US-10-932-182A-70617	Sequence 70617, A
	45	12.8	71.1	25	14	US-11-121-849-36514	Sequence 36514, A

ALIGNMENTS

RESULT 1
US-10-310-914A-1061199/C
; Sequence 1061199, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes an
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1061199
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1061199

Query Match 77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCCCTCTTCGGA 15
Db 20 CCCCCTCTTCGGA 7

RESULT 2
US-11-121-849-112898
; Sequence 112898, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949

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/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO: 112898
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-112898
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Query Match          77.8%; Score 14; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      6  CCCTCTCTGATA 19
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US-11-101-244-1578545
/ Sequence 1578545, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO: 1578545
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1578545
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Query Match          76.7%; Score 13.8; DB 12; Length 19;
Best Local Similarity 64.7%; Pred. No. 8.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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Qy      1  CCCCCCTCTCTGATA 17
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Db      1  CCACCTCCTCTGATA 17
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RESULT 4
US-11-083-784-1578545
/ Sequence 1578545, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
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/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO: 1578545
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1578545
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Query Match          76.7%; Score 13.8; DB 13; Length 19;
Best Local Similarity 64.7%; Pred. No. 8.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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Qy      1  CCCCCCTCTCTGATA 17
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Db      1  CCACCTCCTCTGATA 17
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US-11-121-849-325988
/ Sequence 325988, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
/ FILE REFERENCE: 3684.1
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR FILING DATE: 2004-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO: 325988
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-325988
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Query Match          76.7%; Score 13.8; DB 14; Length 25;
Best Local Similarity 88.2%; Pred. No. 9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1  CCCCCCTCTCTGATA 17
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Db      7  CTCCCTCTCTGAGA 23
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RESULT 6
US-11-136-527-352597/c
/ Sequence 352597, Application US/11136527
/ Publication No. US20050287570A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mount, William M
/ TITLE OF INVENTION: Probe Arrays for Expression Profiling of Rat Genes
/ FILE REFERENCE: 031896-041000 (AM101086)
/ CURRENT FILING DATE: 2005-05-27
/ PRIOR FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US 60/574,294
/ PRIOR FILING DATE: 2005-05-26
/ NUMBER OF SEQ ID NOS: 362830
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 352597
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Probe
US-11-136-527-352597
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Query Match          76.7%; Score 13.8; DB 14; Length 25;
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Best Local Similarity 88.2%; Pred. No. 9e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCCCTTCTGGATAC 18
Db 22 CCACCTCGCTGGATAC 6

RESULT 7

US-11-136-527-352621/c
; Sequence 352621, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 352621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-352621

Query Match
Best Local Similarity 88.2%; Score 13.8; DB 14; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCCCTTCTGGATAC 18
Db 19 CCACCTCGCTGGATAC 3

RESULT 8

US-11-136-527-352632/c
; Sequence 352632, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 352632
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-352632

Query Match
Best Local Similarity 88.2%; Score 13.8; DB 14; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCCCTTCTGGATAC 18
Db 17 CCACCTCGCTGGATAC 1

RESULT 9

US-10-310-914A-908031/c
; Sequence 908031, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an

; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 908031
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-908031

Query Match
Best Local Similarity 93.3%; Score 13.4; DB 8; Length 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCCCTTCTGGA 15
Db 17 CCCCCCTTCTGGA 3

RESULT 10

US-10-310-914A-84927
; Sequence 84927, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84927
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-84927

Query Match
Best Local Similarity 74.4%; Score 13.4; DB 8; Length 24;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCCCTTCTGGA 15
Db 6 CCCCCCTTCTGGA 20

RESULT 11

US-11-121-849-394245/c
; Sequence 394245, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 394245

/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-394245

Query Match 74.4%; Score 13.4; DB 14; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCCCCTCTGTGATAC 17
Db 24 CCGCCTCTGTGATAC 10

RESULT 12
US-10-310-914A-1353078/c
/ Sequence 1353078, Application US/10310914A
/ Publication No. US2006003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kiyazat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1353078
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1353078

Query Match 73.3%; Score 13.2; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTGTGATAC 18
Db 19 CCGCCTCTGTGCTTAC 2

RESULT 13
US-11-101-244-1473850
/ Sequence 1473850, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1473850
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1473850

Query Match 73.3%; Score 13.2; DB 12; Length 19;
Best Local Similarity 61.1%; Pred. No. 1.8e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTGTGATAC 18
Db 2 CACCCACUUCUGUAC 19

RESULT 14
US-11-083-784-1473850
/ Sequence 1473850, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1473850
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1473850

Query Match 73.3%; Score 13.2; DB 13; Length 19;
Best Local Similarity 61.1%; Pred. No. 1.8e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTGTGATAC 18
Db 2 CACCCACUUCUGUAC 19

RESULT 15
US-10-770-726-11899/c
/ Sequence 11899, Application US/10770726
/ Publication No. US20050266409A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Brown, Eugene
/ APPLICANT: Liu, Wei
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATI
/ TITLE OF INVENTION: CANCERS
/ FILE REFERENCE: AM101079 (031896-010000)
/ CURRENT APPLICATION NUMBER: US/10/770,726
/ CURRENT FILING DATE: 2004-02-04
/ NUMBER OF SEQ ID NOS: 48640
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 11899
/ LENGTH: 21
/ TYPE: RNA
/ ORGANISM: RNA1
US-10-770-726-11899

Query Match 73.3%; Score 13.2; DB 8; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCCCTCTGTGATAC 18
Db 20 CCGCCTCTGTGACAC 3

Mon Apr 10 08:45:42 2006

us-10-659-980a-5.sz30.rnpbn

Page 5

Search completed: April 7, 2006, 09:05:20
Job time : 780.324 secs

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OM nucleic - nucleic search, using SW model

Run on: April 7, 2006, 08:38:51 ; Search time 340.054 Seconds

(without alignments)
437.721 Million cell updates/sec

Title: US-10-659-980A-5

Perfect score: 18

Sequence: 1 cccccctctcgtgac 18

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Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 10535742

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-659-948A-5	Sequence 5, Appl1
2	18	100.0	18	US-10-659-980A-5	Sequence 5, Appl1
3	18	100.0	18	US-10-659-983A-5	Sequence 5, Appl1
4	14.4	80.0	25	US-10-719-956-558629	Sequence 74, Appl1
5	14.4	80.0	30	US-09-320-337-74	Sequence 21, Appl1
6	13.8	76.7	18	US-10-659-948A-21	Sequence 21, Appl1
7	13.8	76.7	18	US-10-659-980A-21	Sequence 21, Appl1
8	13.8	76.7	18	US-10-659-983A-21	Sequence 21, Appl1
9	13.8	76.7	25	US-10-719-956-25535	Sequence 25535, A
10	13.8	76.7	25	US-10-719-956-50560	Sequence 50560, A
11	13.8	76.7	28	US-10-169-368-13	Sequence 13, Appl1
12	13.4	74.4	25	US-10-719-956-94288	Sequence 94288, A
13	13.4	74.4	25	US-10-719-956-470164	Sequence 470164, A
14	13.4	74.4	25	US-10-719-956-338352	Sequence 338352, A
15	13.4	74.4	25	US-10-809-189-416880	Sequence 416880, A
16	13.4	74.4	25	US-10-809-189-416880	Sequence 416880, A
17	13.4	74.4	25	US-11-060-756-202014	Sequence 202014, A
18	13.4	74.4	25	US-11-060-756-286165	Sequence 286165, A
19	13.2	73.3	20	US-10-492-928A-288	Sequence 288, App
20	13.2	73.3	25	US-10-719-956-690676	Sequence 690676, A
21	13.2	73.3	25	US-10-719-900-84801	Sequence 84801, A
22	13.2	73.3	27	US-10-921-590-113	Sequence 113, App
23	13.2	73.3	28	US-10-492-928A-282	Sequence 282, App

C	24	13.2	73.3	30	7	US-10-282-122A-78603	Sequence 78603, A
C	25	13	72.2	25	7	US-10-719-956-117959	Sequence 117959, A
C	26	13	72.2	25	7	US-10-719-956-193006	Sequence 193006, A
C	27	13	72.2	25	7	US-10-719-956-511003	Sequence 511003, A
C	28	13	72.2	25	7	US-10-719-956-611802	Sequence 611802, A
C	29	13	72.2	25	8	US-10-719-900-316050	Sequence 316050, A
C	30	13	72.2	25	8	US-10-719-900-574815	Sequence 574815, A
C	31	13	72.2	25	10	US-11-060-756-197597	Sequence 197597, A
C	32	13	72.2	25	10	US-11-060-756-197598	Sequence 197598, A
C	33	12.8	71.1	17	6	US-10-459-876-17	Sequence 17, Appl1
C	34	12.8	71.1	25	5	US-10-098-263B-37037	Sequence 37037, A
C	35	12.8	71.1	25	7	US-10-719-956-89806	Sequence 89806, A
C	36	12.8	71.1	25	7	US-10-719-956-558628	Sequence 558628, A
C	37	12.8	71.1	25	8	US-10-719-900-28087	Sequence 28087, A
C	38	12.8	71.1	25	8	US-10-719-900-226025	Sequence 226025, A
C	39	12.8	71.1	25	8	US-10-719-900-308249	Sequence 308249, A
C	40	12.8	71.1	25	8	US-10-719-900-550905	Sequence 550905, A
C	41	12.8	71.1	25	8	US-10-719-900-627829	Sequence 627829, A
C	42	12.8	71.1	25	8	US-10-719-900-761202	Sequence 761202, A
C	43	12.8	71.1	25	8	US-10-719-900-904924	Sequence 904924, A
C	44	12.8	71.1	25	8	US-10-719-900-949533	Sequence 949533, A
C	45	12.8	71.1	25	9	US-10-809-189-56205	Sequence 56205, A

ALIGNMENTS

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RESULT 1
US-10-659-948A-5
; Sequence 5, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Probe
US-10-659-948A-5
Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CQ 1 CCCCCCTTCTGATAC 18
Db 1 CCCCCCTTCTGATAC 18
RESULT 2
US-10-659-980A-5
; Sequence 5, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
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/ CURRENT FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: US 09/573,684
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 60/386,217
/ PRIOR FILING DATE: 2002-09-19
/ PRIOR APPLICATION NUMBER: US 60/386,218
/ PRIOR FILING DATE: 2002-09-19
/ PRIOR APPLICATION NUMBER: US 60/386,219
/ PRIOR FILING DATE: 2002-09-19
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 5
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide Probe
US-10-659-980a-5
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Query Match      100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCCCCCTCTTGATAC 18
    |||||
DB 1 CCCCCCTCTTGATAC 18
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RESULT 3
US-10-659-983a-5
/ Sequence 5, Application US/106559983A
/ Publication No. US20040157313A1
/ GENERAL INFORMATION:
/ APPLICANT: Hovanec, Timothy A
/ TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
/ FILE REFERENCE: 81289-284779
/ CURRENT APPLICATION NUMBER: US/10/659,983A
/ CURRENT FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: US 09/573,684
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 60/386,217
/ PRIOR FILING DATE: 2002-09-19
/ PRIOR APPLICATION NUMBER: US 60/386,218
/ PRIOR FILING DATE: 2002-09-19
/ PRIOR APPLICATION NUMBER: US 60/386,219
/ PRIOR FILING DATE: 2002-09-19
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 5
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide Probe
US-10-659-983a-5
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Query Match      100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CCCCCCTCTTGATAC 18
    |||||
DB 1 CCCCCCTCTTGATAC 18
```

```
RESULT 4
US-10-719-956-558629
/ Sequence 558629, Application US/10719956
/ Publication No. US20040146910A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
```

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/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002-11-20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 558629
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-719-956-558629
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Query Match      80.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 CCCCCCTCTTGAT 16
    |||||
DB 4 CCCCCCTCTTGAT 19
```

```
RESULT 5
US-09-320-337-74/c
/ Sequence 74, Application US/09320337
/ Patent No. US20010016352A1
/ GENERAL INFORMATION:
/ APPLICANT: Bohinski, Robert J.,
/ APPLICANT: White, Jeffrey A.
/ TITLE OF INVENTION: Nucleic Acid Sequences Controlling
/ TITLE OF INVENTION: Lung Cell - Specific Gene Expression
/ NUMBER OF SEQUENCES: 76
/ CORRESPONDENCE ADDRESSES:
/ ADDRESS: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
/ STREET: 6 Becker Farm Road
/ CITY: Roseland
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch diskette
/ COMPUTER: IBM P160
/ OPERATING SYSTEM: WINDOWS 95
/ SOFTWARE: MS WORD 97
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/320,337
/ FILING DATE: 26-MAY-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/442,809
/ FILING DATE: 17-MAY-1995
/ APPLICATION NUMBER: 08/245,356
/ FILING DATE: 18-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Olstein, Elliot M.
/ REGISTRATION NUMBER: 24,025
/ REFERENCE/DOCKET NUMBER: 271010-447
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 973-994-1700
/ TELEFAX: 973-994-1744
/ INFORMATION FOR SEQ ID NO: 74:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: oligonucleotide
US-09-320-337-74
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```
Query Match      80.0%; Score 14.4; DB 3; Length 30;
Best Local Similarity 93.8%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 CCCCCCTCTTGAT 17
```

Db 24 CCCCTCTCTGATGATA 9

RESULT 6

US-10-659-948A-21
; Sequence 21, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-659-948A-21

Query Match 76.7%; Score 13.8; DB 7; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CCCCTCTCTGATGATC 18
Db 2 CCCCACTTCTGACAC 18

RESULT 7

US-10-659-980A-21
; Sequence 21, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT FILING DATE: US/10/659,980A
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-659-980A-21

Query Match 76.7%; Score 13.8; DB 7; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCTCTCTGATGATC 18
Db 2 CCCCACTTCTGACAC 18

RESULT 8

US-10-659-983A-21
; Sequence 21, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT FILING DATE: US/10/659,983A
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-659-983A-21

Query Match 76.7%; Score 13.8; DB 7; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCTCTCTGATGATC 18
Db 2 CCCCACTTCTGACAC 18

RESULT 9

US-10-719-956-25535
; Sequence 25535, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT FILING DATE: US/10/719,956
; PRIOR APPLICATION NUMBER: 2003-11-20
; PRIOR FILING DATE: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 25535
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-25535

Query Match 76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTCTCTGATGATA 17
Db 3 CCCTCTCTCTGATGATA 19

RESULT 10
US-10-719-956-50560/c

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/ Sequence 50560, Application US/10719956
/ Publication No. US20040146910A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ PRIOR FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 50560
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-719-956-50560
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Query Match 76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY 2 CCCCCTCTTGATGATAC 18
DB 19 CCACCTCGCTGGATAC 3
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```
RESULT 11
US-10-169-368-13/C
/ Sequence 13, Application US/10169368
/ Publication No. US20050070001A1
/ GENERAL INFORMATION:
/ APPLICANT: Kleelek, Knut
/ APPLICANT: Brinkmann, Thomas
/ APPLICANT: Goetting, Christian
/ APPLICANT: Kuhn, Joachim
/ TITLE OF INVENTION: Xylosyltransferase and isoforms thereof
/ FILE REFERENCE: 020195-00002
/ CURRENT APPLICATION NUMBER: US/10/169,368
/ PRIOR FILING DATE: 2002-07-01
/ PRIOR APPLICATION NUMBER: PCT/EP00/13311
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 28
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-169-368-13
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Query Match 76.7%; Score 13.8; DB 9; Length 28;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY 2 CCCCCTCTTGATGATAC 18
DB 21 CCCCCTCTTGATGATAC 5
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RESULT 12
US-10-719-956-94288
/ Sequence 94288, Application US/10719956
/ Publication No. US20040146910A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ PRIOR FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002 11 20
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/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 94288
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-719-956-94288
```

```
Query Match 74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 CCCCCTCTTGATGATAC 15
DB 4 CCCCCTCTTGATGATAC 18
```

```
RESULT 13
US-10-719-956-470164
/ Sequence 470164, Application US/10719956
/ Publication No. US20040146910A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ PRIOR FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 470164
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-719-956-470164
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Query Match 74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY 3 CCCCCTCTTGATGATAC 17
DB 11 CCCCCTCTTGATGATAC 25
```

```
RESULT 14
US-10-719-900-338352/C
/ Sequence 338352, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ PRIOR FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 338352
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-338352
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```
Query Match 74.4%; Score 13.4; DB 8; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY 4 CCCCCTCTTGATGATAC 18
DB 22 CCCCCTCTTGATGATAC 8
```

RESULT 15
US-10-719-900-416880

; Sequence 416880, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 416880
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-416880

Query Match 74.4%; Score 13.4; DB 8; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CCCTCTTCGATAC 18
Db 4 CCCTCTTCGAGAC 18

Search completed: April 7, 2006, 09:48:01
Job time : 341.054 secs

;

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:38:52 ; Search time 63.2432 Seconds

(without alignments)
505.921 Million cell updates/sec

Title: US-10-659-980A-5

Sequence: 1 ccccccctctcgcgatac 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1026780

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/prodata/1/ina/5/COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A/COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B/COMB.seq:*
5: /cgn2_6/prodata/1/ina/H/COMB.seq:*
6: /cgn2_6/prodata/1/ina/PCTUS/COMB.seq:*
7: /cgn2_6/prodata/1/ina/PP/COMB.seq:*
8: /cgn2_6/prodata/1/ina/RE/COMB.seq:*
9: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.4	80.0	30	2	US-08-442-809A-74
C 2	13.4	74.4	25	3	US-09-396-196G-81113
C 3	12.8	71.1	17	3	US-09-583-610D-17
C 4	12.8	71.1	25	3	US-09-396-196G-56205
C 5	12.4	68.9	20	3	US-09-198-452A-2493
C 6	12.4	68.9	25	3	US-08-943-731-305
C 7	12.4	68.9	25	3	US-09-396-196G-24325
C 8	12.4	68.9	25	3	US-09-396-196G-45539
C 9	12.2	67.8	23	2	US-07-722-798A-77
C 10	12.2	67.8	25	3	US-09-396-196G-20092
C 11	12.2	67.8	25	3	US-09-396-196G-20103
C 12	12.2	67.8	27	2	US-08-480-473B-78
C 13	12.2	67.8	27	3	US-08-915-213-28
C 14	12.2	67.8	27	3	US-09-235-211-28
C 15	12.2	67.8	27	6	PCT-US96-10251-28
C 16	12.2	67.8	20	2	US-08-173-489C-17
C 17	12.2	66.7	20	3	US-10-002-623-451
C 18	11.8	65.6	18	3	US-09-289-377-10
C 19	11.8	65.6	20	3	US-09-495-714C-106
C 20	11.8	65.6	24	2	US-08-621-564B-3
C 21	11.8	65.6	24	3	US-09-269-220-3
C 22	11.8	65.6	25	3	US-09-538-709-290
C 23	11.8	65.6	25	3	US-09-396-196G-84823
C 24	11.6	64.4	23	2	US-07-722-798A-78

C 25	11.6	64.4	25	3	US-09-866-108A-11865	Sequence 11865, A
C 26	11.6	64.4	25	3	US-09-866-108A-11866	Sequence 11866, A
C 27	11.6	64.4	25	3	US-09-866-108A-11867	Sequence 11867, A
C 28	11.6	64.4	25	3	US-09-866-108A-11868	Sequence 11868, A
C 29	11.6	64.4	25	3	US-09-866-108A-11869	Sequence 11869, A
C 30	11.6	64.4	25	3	US-09-866-108A-11870	Sequence 11870, A
C 31	11.6	64.4	25	3	US-09-866-108A-11871	Sequence 11871, A
C 32	11.6	64.4	25	3	US-09-866-108A-11872	Sequence 11872, A
C 33	11.6	64.4	25	3	US-09-396-196G-10214	Sequence 10214, A
C 34	11.6	64.4	25	3	US-09-396-196G-103965	Sequence 103965, A
C 35	11.6	64.4	25	3	US-09-396-196G-103966	Sequence 103966, A
C 36	11.6	64.4	27	3	US-09-688-017-336	Sequence 336, App
C 37	11.6	64.4	30	2	US-08-479-817-1	Sequence 1, Appl1
C 38	11.6	64.4	30	2	US-08-461-038-1	Sequence 1, Appl1
C 39	11.6	64.4	30	2	US-08-461-645-1	Sequence 1, Appl1
C 40	11.6	64.4	30	3	US-08-221-543-1	Sequence 1, Appl1
C 41	11.6	64.4	30	3	US-09-451-905-42	Sequence 42, Appl
C 42	11.4	63.3	17	3	US-08-584-040-5423	Sequence 5423, Ap
C 43	11.4	63.3	17	3	US-09-371-772B-2322	Sequence 2322, Ap
C 44	11.4	63.3	18	3	US-09-685-664B-2322	Sequence 2322, Ap
C 45	11.4	63.3	18	3	US-09-474-922A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-442-809A-74/C
; Sequence 74, Application US/08442809A
; Patent No. 5976873
; GENERAL INFORMATION:
; APPLICANT: Bohinski, Robert J.,
; APPLICANT: Whitsett, Jeffrey A.,
; TITLE OF INVENTION: Nucleic Acid Sequences
; TITLE OF INVENTION: Controlling Lung Cell -
; TITLE OF INVENTION: Specific Gene Expression
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Carella, Byrne, Baln, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442, 809A
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,356
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; US-08-442-809A-74

Query Match 80.0%; Score 14.4; DB 2; Length 30;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCCCTCTCTGGATA 17
Db 24 CCCCCTCTCTGGATA 9

RESULT 2
US-09-396-196G-81113/C
; Sequence 81113, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-81113

Query Match 74.4%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCCCTCTCTGGATA 17
Db 23 CCCCCTCTCTGGATA 9

RESULT 3
US-09-583-610D-17
; Sequence 17, Application US/09583610D
; Patent No. 6740735
; GENERAL INFORMATION:
; APPLICANT: Glanville, S.H.
; APPLICANT: Bradley, W.A.
; TITLE OF INVENTION: DNA Encoding Human apob48r: A Monocyte-Macrophage
; TITLE OF INVENTION: Apolipoprotein B48 Receptor Gene and Protein
; FILE REFERENCE: D5880CIP
; CURRENT APPLICATION NUMBER: US/09/583,610D
; CURRENT FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/130,242
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense primers were based on the 5'-end
; OTHER INFORMATION: sequence of the THP-1 (73 clone (bp 2203-2187
US-09-583-610D-17

Query Match 71.1%; Score 12.8; DB 3; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCCTCTCTGGAT 16
Db 1 CCAGCCTCTCTGGAT 16

RESULT 4
US-09-396-196G-56205/C
; Sequence 56205, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56205
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-56205

Query Match 71.1%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCCTCTCTGGATA 17
Db 23 CCCCCTCTCTGGATA 8

RESULT 5
US-09-198-452A-2493
; Sequence 2493, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffith, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2493
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2493

Query Match 68.9%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCTCTCTGGATAC 18
Db 4 CCTCTCTGGATTC 17

RESULT 6
US-08-943-731-305/C
; Sequence 305, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILIA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL

APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KOKKO, JARMO
APPLICANT: ALA-KOKKO, LENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
ADDRESSER: PANTICH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7066
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 8311494
INFORMATION FOR SEQ ID NO: 305:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-305

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCCTCTCTGGAT 16
Db 24 CCCCTCTCTGGAT 11

RESULT 7
US-09-396-196G-24325
Sequence 24325, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 24325
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-24325

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCCCTCTCTGGATA 17
Db 3 CCCCTCTCTGGAGA 16

RESULT 8
US-09-396-196G-45539
Sequence 45539, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45539
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-45539

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCCCTCTCTGGATA 17
Db 1 CCCACTCTCTGGATA 14

RESULT 9
US-07-722-798A-77
Sequence 77, Application US/07722798A
Patent No. 5427930
GENERAL INFORMATION:
APPLICANT: Larry G. Birkenmeyer
APPLICANT: John J. Carrino
APPLICANT: Bruce J. Dille
APPLICANT: Hsiang-Yun Hu
APPLICANT: Jon David Kratochvil
APPLICANT: Thomas G. Laffier
APPLICANT: Ronald L. Marshall
APPLICANT: Laurie A. Rinhardt
APPLICANT: Natalie A. Solomon
TITLE OF INVENTION: AMPLIFICATION OF TARGET NUCLEIC
NUMBER OF INVENTION: ACIDS USING GAP FILLING LIGASE CHAIN REACTION
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/722,798A
; FILING DATE: 19910628
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-4884
; TELEFAX: 708-937-9556
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-07-722-798A-77

```

```

Query Match 67.8%; Score 12.2; DB 2; Length 23;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 2 CCCCTCTTCTGGATAC 18
Db 1 CCCCTGTCTGTGTTCC 17

```

```

RESULT 10
US-09-396-196G-20092/C
; Sequence 20092, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-20092

```

```

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 2 CCCCTCTTCTGGATAC 18
Db 20 CCACCTCGCTGGATAC 4

```

```

RESULT 11
US-09-396-196G-20103/C
; Sequence 20103, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.

```

```

; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-20103

```

```

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 2 CCCCTCTTCTGGATAC 18
Db 18 CCACCTCGCTGGATAC 2

```

```

RESULT 12
US-08-480-473B-28/C
; Sequence 28, Application US/08480473B
; Patent No. 5882914
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,473B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/053001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-480-473B-28

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Qy 1 CCCCTCTTCTGGATAC 17
Db 27 CCCCTCTTCTGGATAC 11

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Query Match 67.8%; Score 12.2; DB 2; Length 27;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 13

US-08-915-213-28/c
Sequence 28, Application US/08915213
Patent No. 6020462
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,213
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-915-213-28

Query Match 67.8%; Score 12.2; DB 3; Length 27;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCCTTCTGATA 17
DB 27 CCCCCCTTTCAGATA 11

RESULT 14
US-09-235-217-28/c
Sequence 28, Application US/09235217
Patent No. 6222018
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,217

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-235-217-28

Query Match 67.8%; Score 12.2; DB 3; Length 27;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCCTTCTGATA 17
DB 27 CCCCCCTTTCAGATA 11

RESULT 15
PCT-US96-10251-28/c
Sequence 28, Application PC/TUS9610251
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10251
FILING DATE: 06-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US96-10251-28

Query Match 67.8%; Score 12.2; DB 6; Length 27;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	CCCCCTTCTGGATA	17
Db	27	CCCCCTTTTCAGATA	11

Search completed: April 7, 2006, 08:41:14
Job time : 64.2432 secs

18.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 7, 2006, 08:38:51 ; Search time 2905.78 Seconds
(without alignments)
289.825 Million cell updates/sec

Title: US-10-659-980A-5
Perfect score: 18
Sequence: 1 ccccccctctcgcgtac 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 52094

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	11.8	65.6	22 9	AZ817329 2M0086D22
3	11.8	65.6	28 8	R54679 vJ74e12.r1
4	11.8	65.6	28 9	AZ489682 1M0322G16
5	11.6	64.4	23 9	AZ785027 2M0028H03
6	11.4	63.3	13 5	BQ589768 E012680-0
7	11.4	63.3	26 9	AZ487733 1M0317A10
8	11.2	62.2	22 1	AI039313 0X36P04.8
9	11.2	61.1	19 9	AZ875769 2M0190A02
10	11.1	61.1	20 9	AZ627859 1M0476B04
11	11.1	61.1	25 9	AZ585557 1M0390M18
12	11.1	61.1	26 8	D18736 MUGS01798
13	10.8	60.0	23 9	AZ592213 1M0402P23
14	10.8	60.0	25 1	AI915575 1M040909.x
15	10.8	60.0	28 1	AI649190 uk32d12.x
16	10.8	60.0	29 8	AI649190 uk32d12.x
17	10.8	60.0	30 9	AZ584820 1M0389A14
18	10.8	60.0	30 9	AZ584820 1M0389A14
19	10.6	58.9	23 9	AZ660176 1M0538A12
20	10.6	58.9	25 8	CX007773 1030c09.b
21	10.6	58.9	26 9	AZ835063 2M0129B09
22	10.6	58.9	26 9	AZ835063 2M0129B09

C 23	10.6	58.9	28 9	AZ647874 1M0514D07
C 24	10.6	58.9	30 1	AU251318 AU251318
C 25	10.6	58.9	30 10	C2472794 d02410-5p
C 26	10.4	57.8	17 10	AJ599163 Arabidops
C 27	10.4	57.8	22 8	DR026424 Osmo00431
C 28	10.4	57.8	22 9	AZ982662 2M0263J06
C 29	10.4	57.8	24 9	AZ404465 1M0172P09
C 30	10.4	57.8	24 11	TA185C06P
C 31	10.4	57.8	25 1	AI628239 T. Brucei
C 32	10.4	57.8	26 1	AU265518 AU265518
C 33	10.4	57.8	27 9	AZ776617 2M0010D23
C 34	10.4	57.8	28 9	BH903856 SALK_1035
C 35	10.4	57.8	29 5	BQ590098 E012643-0
C 36	10.4	57.8	29 9	AZ307991 1M0010F01
C 37	10.4	57.8	30 5	BQ590438 E012839-0
C 38	10.4	57.8	30 9	AZ804486 2M0065D07
C 39	10.2	56.7	22 1	AA936014 0826D08.s
C 40	10.2	56.7	25 1	AA894827 0161008.s
C 41	10.2	56.7	25 11	TA115D09Q
C 42	10.2	56.7	26 10	AG203573 Pan tlog1
C 43	10.2	56.7	28 1	AA905471 OK01E11.8
C 44	10.2	56.7	28 9	AZ853408 2M0156P01
C 45	10.2	56.7	28 10	CL663977 PRI0145d_

ALIGNMENTS

RESULT 1
TA25G06P/c 26 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 25g06, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL453426 GI:11849213
VERSION AL453426.1 GI:11849213
KEYWORDS GSS.

SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrett, B.G.
TITLE Direct Submision
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrett@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..26
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="25g06"

ORIGIN

Query Match 67.8%; Score 12.2; DB 11; Length 26;
Best Local Similarity 82.4%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 CGCCCTCTCTGAT 11

RESULT 4
 A2489682/c 28 bp DNA 1linear GSS 05-OCT-2000
 LOCUS 1M032G16P Mouse 10kb plasmid UGCLM1 library Mus musculus genomic
 DEFINITION clone UGCLM032G16 P, genomic survey sequence.
 ACCESSION A2489682
 VERSION A2489682.1 GI:10659670
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0322 ROW: G Column: 16
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM032G16"
 /sex="Male"
 /lab_host="B. Col1 strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCLM1 library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.6%; Score 11.8; DB 9; Length 28;
 Best Local Similarity 86.7%; Pred. No. 3.9e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 0Y 1 CCCCTCTCTGGA 15

Db 18 CCCCTCTCTGGA 4

RESULT 5
 CZ443094
 LOCUS 28 bp DNA 1linear GSS 07-APR-2005
 DEFINITION 1BB8D03.fwd HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells Homo sapiens genomic clone
 1BB8D03.fwd, genomic survey sequence.
 ACCESSION CZ443094
 VERSION CZ443094.1 GI:62379366
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 28)
 Lewinski, M.K., Bisgrove, D., Shin, P., Chen, H., Hoffmann, C., Hammenhall, S., Verdin, E., Berry, C.C., Ecker, J.R. and Bushman, F.D.
 Genome-wide analysis of chromosomal features repressing human immunodeficiency virus transcription
 J. Virol. 79 (11), 6610-6619 (2005)
 15890895
 Contact: Bushman FD
 Department of Microbiology
 University of Pennsylvania School of Medicine
 402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA
 Tel: 215 573 8732
 Fax: 215 573 4856
 Email: bushman@mail.med.upenn.edu
 Class: PCR with specific primers.
 Location/Qualifiers
 1..28
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="1BB8D03.fwd"
 /cell_line="Jurkat"
 /clone_1lb="HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells"
 /note="Vector: LTR-Tat-IREs-GFP (pBV711); We have investigated regulatory sequences in noncoding human DNA that are associated with repression of an integrated human immunodeficiency virus type 1 (HIV-1) promoter. HIV-1 integration results in the formation of precise and homogeneous junctions between viral and host DNA, but integration takes place at many locations. Thus, the variation in HIV-1 gene expression at different integration sites reports the activity of regulatory sequences at nearby chromosomal positions. Negative regulation of HIV transcription is of particular interest because of its association with maintaining HIV in a latent state in cells from infected patients. To identify chromosomal regulators of HIV transcription, we infected Jurkat T cells with an HIV-based vector transducing green fluorescent protein (GFP) and separated cells into populations containing well-expressed (GFP-positive) or poorly expressed (GFP-negative) proviruses. We then determined the chromosomal locations of the two classes by sequencing 971 junctions between viral and cellular DNA. Possible effects of endogenous cellular transcription were characterized by transcriptional profiling. Low-level GFP expression correlated with integration in (i) gene deserts, (ii) centromeric heterochromatin, and (iii) very highly expressed cellular genes. These data provide a genome-wide picture of chromosomal features that repress transcription and suggest models for transcriptional latency in cells from HIV-infected patients."

ORIGIN

Query Match 65.6%; Score 11.8; DB 10; Length 28;
 Best Local Similarity 86.7%; Pred. No. 3.9e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 CCCCTCTTCTGATA 17
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 DB 14 CCCCTCTTCTAGTGA 28

RESULT 6
 A2785027/c 23 bp DNA linear GSS 16-FEB-2001

LOCUS 2M0028H03R Mouse 10kb plasmid UUGCM library Mus musculus genomic
 DEFINITION clone UUGC2M0028H03 R, genomic survey sequence.

ACCESSION A2785027
 VERSION A2785027.1 GI:12921357
 KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: bdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0028 row: H column: 03
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES
 source 1..23

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0028H03"
 /sex="Male"
 /lab_host="R. Colt strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCM library"
 /note="Vector: pMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 64.4%; Score 11.6; DB 9; Length 23;
 Best Local Similarity 77.8%; Pred. No. 4.8e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCCCCTCTCTGATAC 18
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 DB 20 CCCCCCTCAGCTGAGAC 3

RESULT 7

B0589768

LOCUS B0589768 13 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012680-024-020-D03-SP6 MP12-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-020-D03 5-PRIME, mRNA sequence.

ACCESSION B0589768
 VERSION B0589768.1 GI:26119351
 KEYWORDS EST.

ORGANISM Beta vulgaris

SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 13)
 Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wuck, W., Menze, A., O'Brien, J., Leinrich, H.
 and Radloff, U.

TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)

COMMENT

ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 13 Std Error: 0.00
 Plate: 20 row: D column: 03
 Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
 Location/Qualifiers

FEATURES
 source 1..13

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 /cultiivar="KWS2320 (double haploid, monogerm breeding
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 /db_xref="GABI:190356"
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 /clone="024-020-D03"
 /clone_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet. Library provided by KWS
 Kleinfeldener Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 63.3%; Score 11.4; DB 5; Length 13;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CCCCTCTTCTGAT 16
 |||||
 DB 1 CCCTCTTCTTGAAT 13

ORIGIN

RESULT 8
 AZ487733
 LOCUS
 DEFINITION 26 bp DNA linear GSS 05-OCT-2000
 1M0317A10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0317A10 R, genomic survey sequence.
 ACCESSION
 AZ487733
 VERSION
 AZ487733.1 GI:10655751
 GSS.
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0317 row: A column: 10
 Seq primer: CACACGGAACACGATACACC
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0317A10"
 /sex="Male"
 /lab_host="R. Co1 strain XL10-Gold, T1-resistant, F-"
 /clone_jib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: pMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 63.3%; Score 11.4; DB 9; Length 26;
 Best Local Similarity 92.3%; Pred. No. 6.1e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 4 CCGCTTCTGGAT 16
 |||||
 Db 10 CCGCTTCTGGAT 22

RESULT 9
 A1039313
 LOCUS
 DEFINITION 22 bp mRNA linear EST 24-SEP-1998
 0X36D04.s1 Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone
 IMAGE:1658383 3' similar to SW-TP33_HUMAN p49746 THROMBOSPONDIN 3
 PRECURSOR, contains Alu repetitive element, mRNA sequence.
 ACCESSION
 A1039313
 VERSION
 A1039313.1 GI:3278507
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 1 (bases 1 to 22)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 TITLE
 Unpublished (1997)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 This clone is available royalty-free through LINT; contact the
 IMAGE Consortium (info@image.jnl.gov) for further information.
 Insert length: 954 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amerham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source
 1..22
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1658383"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /clone_jib="Soares total_fetus_Nb2HP8_9w"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from pooled 8-9 week
 (total) fetus material with a Not I - oligo(dT) primer [5'
 TGTTCACATCGAAGTGGAGCGCCCTTAATTTTCTTTTCTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptor
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 62.2%; Score 11.2; DB 1; Length 22;
 Best Local Similarity 81.2%; Pred. No. 7.6e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 CCGCCCTTCTGGAT 16
 |||||
 Db 5 CCGCCCTTCTGGAT 20
 RESULT 10
 A2875769
 LOCUS
 DEFINITION 19 bp DNA linear GSS 21-FEB-2001
 2M0190A02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGC2M0190A02 R, genomic survey sequence.
 ACCESSION
 A2875769
 VERSION
 A2875769.1 GI:13086107
 GSS.
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

TITLE
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0190 row: A column: 02
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0190A02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 61.1%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTGGA 15
|||||
Db 1 CCTCTTCTGGA 11

RESULT 11
AZ627859 20 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0476B04F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
DEFINITION clone UUCGCM0476B04 F, genomic survey sequence.
ACCESSION AZ627859
VERSION AZ627859.1 GI:11750145
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: E column: 04
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0476B04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 61.1%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCTTCTGG 14
|||||
Db 3 CCTCTTCTGG 13

RESULT 12
AZ585557 25 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0390M18R Mouse 10kb plasmid UUCGCM library Mus musculus genomic
DEFINITION clone UUCGCM0390M18 R, genomic survey sequence.
ACCESSION AZ585557
VERSION AZ585557.1 GI:11707559
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0390 row: M column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
FEATURES
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0390M18"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 61.1%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 4 CCGCTTCTGG 14
|||||
Db 20 CCGCTTCTGG 10

RESULT 13
LOCUS D18736 26 bp mRNA linear EST 09-FEB-2005
DEFINITION MUSGS01798 Mouse 3'-directed Mus musculus cDNA clone md0836 3',
mRNA sequence.
ACCESSION D18736
VERSION D18736.1 GI:1100705
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 26)
AUTHORS
Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
TITLE
Analysis of gene expression in mouse embryogenesis by 3'-directed
cDNA sequencing
JOURNAL
Unpublished (1995)
CONTACT: Shoko Kawamoto
Institute for Cellular and Molecular Biology
Osaka University
1-3, Yamadaoka, Suita, Osaka, 565, Japan
Email: shoko@next.imb.osaka-u.ac.jp.
FEATURES
Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="md0836"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
/clone_1ib="Mouse 3'-directed"
ORIGIN
Query Match 61.1%; Score 11; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 6 CTCTTCTGGAT 16
|||||
Db 12 CTCTTCTGGAT 2

RESULT 14
LOCUS AZ592213 23 bp DNA linear GSS 13-DEC-2000
DEFINITION IM040223R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M040223 R, genomic survey sequence.
ACCESSION AZ592213
VERSION AZ592213.1 GI:11714403
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0402 row: P column: 23
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M040223"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"

/clone_11b="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 10.8; DB 9; Length 23;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTCTTCTGGATAC 18
|||||||
DB 3 CCTCTTCTGACAC 16

RESULT 15

AI915575 25 bp mRNA linear EST 28-JUL-1999
LOCUS tr40909.x1 NCI_CGAP_Ov23 Homo sapiens cDNA IMAGE:2220832 3'
DEFINITION simlary to SW:P100 HUMAN P30808 DNA-BINDING P52/P100 COMPLEX, 100
KD SUBUNIT ; contains element MSRI repetitive element ;, mRNA
sequence.

ACCESSION

AI915575
VERSION AI915575.1 GI:5635430

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 25)

NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strauberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www.bio.1nl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2220832"

/tissue type="tumor, 5 pooled (see description)"

/lab_host="DH10B"

/clone_11b="NCI_CGAP_Ov23"
/note="Organ: ovary; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

ORIGIN

Query Match 60.0%; Score 10.8; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCCTTCTTGG 14
|||||||
DB 19 CCCCCCTTCTTGG 6

Search completed: April 7, 2006, 10:30:59
Job time : 2907.78 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 08:38:45 ; Search time 357.081 Seconds
(without alignments)
335.959 Million cell updates/sec

Title: US-10-659-980A-5
Perfect score: 18
Sequence: 1 cccccctcttcgagatc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4936997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 4138570

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N GeneSeq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001s:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	ABA02420
2	18	100.0	18	12	ABA02420
3	14.4	80.0	30	4	AA01828
4	13.8	74.7	18	12	ADW32724
5	13.4	74.4	22	12	ADL32573
6	13.2	73.3	20	10	ADG36420
7	13.2	73.3	27	12	ADG31445
8	13.2	73.3	27	12	ADK41856
9	13.2	73.3	28	10	ADG36414
10	13.2	73.3	30	8	ACA54549
11	13.2	73.3	30	8	ABX13526
12	12.8	71.1	17	10	ADH30251
13	12.8	71.1	17	12	ADG00840
14	12.8	71.1	18	12	ADN08161
15	12.8	71.1	25	9	ACT137046
16	12.6	70.0	24	14	ADZ08754
17	12.4	68.9	17	3	AA02030
18	12.4	68.9	17	3	AA02029

20	12.4	68.9	20	2	AA031192
C	21	12.4	20	6	ABX03745
C	22	12.4	20	13	ABX13323
C	23	12.4	20	12	ADN02302
C	24	12.4	20	13	ADR68924
C	25	12.4	25	5	AA022073
C	26	12.4	25	5	ACT19119
C	27	12.2	17	2	AA017514
C	28	12.2	17	8	ABX65019
C	29	12.2	17	14	ADZ34093
C	30	12.2	18	3	AA014813
C	31	12.2	19	10	ADP36053
C	32	12.2	19	10	ADP36480
C	33	12.2	19	11	ADL79197
C	34	12.2	19	11	ADL78948
C	35	12.2	19	12	ADQ14296
C	36	12.2	19	14	ADY87306
C	37	12.2	19	14	ADY87733
C	38	12.2	20	14	ADZ84877
C	39	12.2	20	14	ADZ84729
C	40	12.2	21	13	ADU42656
C	41	12.2	23	2	AA036081
C	42	12.2	23	2	AA039338
C	43	12.2	23	6	ABK24426
C	44	12.2	23	10	ADR40344
C	45	12.2	24	14	ADW38589

ALIGNMENTS

RESULT 1	ABA02420	ABA02420 standard; DNA; 18 BP.
ID	ABA02420	
XX	ABA02420;	
AC	29-AUG-2003 (revised)	
XX	DT 04-MAR-2002 (first entry)	
XX		Type A/A1 ammonia-oxidising bacterium 16S rRNA gene probe.
DE		
XX		Type A, type A1, ammonia-oxidising bacterium; AOB; nitrite;
KW		16S rRNA gene; ribosomal RNA; aquarium; aquaculture;
KM		waste water treatment; bioremediation; probe; ss.
XX		
OS		Nitrosomonadales.
XX		
PM		WO200190312-A1.
XX		
PD		29-NOV-2001.
XX		
PF		17-MAY-2001; 2001WO-US016265.
XX		
PR		19-MAY-2000; 2000US-00573684.
XX		
PA		(AQUA-) AQUARIA INC.
XX		
PI		Hovaneq TA, Burrell PC,
XX		
DR		WPI; 2002-075367/10.
XX		
PT		New bacteria capable of oxidizing ammonia to nitrite, for preventing or
PT		alleviating the accumulation of ammonia in fresh water aquaria, seawater
XX		aquaria and waste water.
PS		
XX		Claim 26; Page 53; 62pp; English.
CC		The invention relates to 4 novel types of ammonia-oxidising bacteria
CC		(AOB) found in freshwater aquaria. The bacteria are able to oxidise
CC		ammonia to nitrite and are members of the ammonia-oxidising bacteria
CC		family of the beta subdivision of Proteobacteria. The 4 types of bacteria
CC		can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene

CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
 CC R3clone140), type A1 (e.g., R3clone187), type B (e.g., R3clone5) and type
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 CC gene sequences of the ammonia-oxidizing bacteria of the invention.
 CC oligonucleotide probes and primers for the detection of these bacteria,
 CC and compositions comprising the bacteria. The bacteria of the invention
 CC are useful in biological filters for reducing ammonia accumulation in
 CC both freshwater and seawater aquaria. They may also be used in waste
 CC water treatment and in bioremediation processes to reduce the level of
 CC pollution caused by ammonia. The present sequence represents a
 CC specifically claimed probe for the detection of the 16S rRNA gene
 CC sequences of the type A and A1 ammonia-oxidizing bacteria (ABA02416-
 CC ABA02417). (Updated on 29-AUG-2003 to standardise OS field)
 CC XX

SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCTGATAC 18
 DB 1 CCCCCCTCTCTGATAC 18

RESULT 2

ADM32708
 ID ADM32708 standard; DNA; 18 BP.

ADM32708;

17-JUN-2004 (first entry)

DE Nitrospirilla-like 16S rDNA probe. S-G-Nespa-0149-a-A-18.

KW 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;
 KW aqueous environment; freshwater; seawater; aquarium; ss; probe.

OS Nitrospirilla sp.

FN WO2004026772-A2.

PD 01-APR-2004.

PE 10-SEP-2003; 2003WO-US028210.

PR 19-SEP-2002; 2002US-0386217P.

PR 19-SEP-2002; 2002US-0386218P.

PR 19-SEP-2002; 2002US-0386219P.

PA (AQUA-) AQUARIA INC.

PI Hovanec TA;

DR WPI; 2004-304936/28.

XX New composition comprising an isolated bacterial strain that oxidizes
 XX ammonia to nitrite, useful for alleviating or preventing the accumulation
 XX of ammonia in aqueous environment.

PT Example 6; Page 34; 98pp; English.

XX This sequence represents a probe which was used in the detection of 16S
 XX rDNA sequence derived from an ammonia oxidizing bacteria (AOB). The
 XX amplified sequence may be used in a composition which comprises an
 XX isolated bacterial strain that oxidizes ammonia to nitrite. The
 XX composition may be used for alleviating or preventing the accumulation of
 XX ammonia in a medium. The ammonia is reduced by at least 30% when compared
 XX with a level of ammonia that would exist in the absence of the bacterial
 XX strain. The composition is useful for alleviating or preventing the
 XX accumulation of ammonia in aqueous environment, e.g. a freshwater or
 XX seawater aquarium.

SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCCCTCTCTGATAC 18
 DB 1 CCCCCCTCTCTGATAC 18

RESULT 3

AA511828/c
 ID AA511828 standard; DNA; 30 BP.

AA511828;

DT 24-OCT-2001 (first entry)

DE Human surfactant protein B, SPB, TTF-1 containing oligonucleotide Bcm.

KW Human surfactant protein B; SPB; promoter; nuclear protein binding site;
 KW Thyroid transcription factor; TTF-1; lung cancer; thyroid cancer; ds;
 KW Bcm; mutant.

XX Homo sapiens.

OS Synthetic.

FT Key location/Qualifiers

FT mutation replace(10..13,CAAG)

FT /*tag= a

FT /note= "Mutates the TTF-1 binding site"

PN US2001016352-A1.

PD 23-AUG-2001.

PF 26-MAY-1999; 99US-00320337.

PR 18-MAY-1994; 94US-00245356.

PR 17-MAY-1995; 95US-00442809.

PA (BOHI/) BOHINSKI R J.

PA (WHIT/) WHITSETT J A.

PI Bohinski RJ, Whitsett JA;

DR WPI; 2001-513959/56.

XX Oligonucleotide sequences which bind nuclear proteins and surfactants
 XX found in lung cells, useful for detecting cancers that originate in the
 XX lung.

PT Example 5; Fig 34a; 76pp; English.

XX The invention relates to an oligonucleotide which includes at least 1
 XX nucleic acid sequence which binds to at least 1 nuclear protein found in
 XX lung cells (e.g. the thyroid transcription factor 1, TTF-1, protein). The
 XX oligonucleotide can be expressed in lung cells via a vector and can be
 XX used to target therapeutic agents to kill lung or thyroid cancer cells.
 XX The oligonucleotide can be used to detect or diagnose lung or thyroid
 XX cancer. The oligonucleotides may be designed from the sequences of, for
 XX example, the promoters of lung-specific genes such as those encoding
 XX surfactant proteins. The present sequence is a mutated oligonucleotide
 XX from human surfactant protein B, SPB, promoter used in an EMSA
 XX (electrophoretic mobility shift assay) assay to confirm the presence of
 XX TTF-1 binding sites in the SPB promoter. The TTF-1 site has been mutated

SQ Sequence 30 BP; 6 A; 6 C; 12 G; 6 T; 0 U; 0 Other;
 Query Match 80.0%; Score 14.4; DB 4; Length 30;
 Best Local Similarity 93.8%; Pred. No. 2.6e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCCCCCTCTGTGATA 17
 |||||
 DB 24 CCCCCCTCTGTGATA 9

RESULT 4

ID ADM32724 standard; DNA; 18 BP.

AC ADM32724;

DT 17-JUN-2004 (first entry)

DE Nitrosomonas aestuarii-like 16S rDNA probe.

KW 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;
 aqueous environment; freshwater; seawater; aquarium; ss; probe.

OS Nitrosomonas aestuarii.

PN WO2004026772-A2.

PD 01-APR-2004.

PF 10-SEP-2003; 2003WO-US028210.

PR 19-SEP-2002; 2002US-0386217P.

PR 19-SEP-2002; 2002US-0386218P.

PA (AQUA-) AQUARIA INC.

PI Hovanec TA;

DR WPI; 2004-304936/28.

PT New composition comprising an isolated bacterial strain that oxidizes
 ammonia to nitrite, useful for alleviating or preventing the accumulation
 of ammonia in aqueous environment.

PS Claim 10; Page 34; 98pp; English.

CC This sequence represents a probe which was used in the detection of 16S
 rDNA sequence derived from an ammonia oxidizing bacteria (AOB). The
 amplified sequence may be used in a composition which comprises an
 isolated bacterial strain that oxidizes ammonia to nitrite. The
 composition may be used for alleviating or preventing the accumulation of
 ammonia in a medium. The ammonia is reduced by at least 30% when compared
 with a level of ammonia that would exist in the absence of the bacterial
 strain. The composition is useful for alleviating or preventing the
 accumulation of ammonia in aqueous environment, e.g. a freshwater or
 seawater aquarium.

SQ Sequence 18 BP; 3 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 12; Length 18;

Best Local Similarity 88.2%; Pred. No. 5e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCCCCCTCTGTGATA 18
 |||||
 DB 2 CCCCCCTCTGTGACAC 18

RESULT 5

ID AAH42343/C

AC AAH42343 standard; DNA; 28 BP.

DT 17-SEP-2001 (first entry)

DE PCR primer for human xylosyltransferase (XT) isoform XT-I cDNA.

KW UDP-xylose:proteoglycan core protein beta-D-xylosyltransferase; XT;

KW XT-I; XT-II; glycosaminoglycan; sclerotic disease; PCR primer;

OS chronic inflammatory joint disease; diagnostic marker; gene marker; ss.

PN WO200149831-A2.

PD 12-JUL-2001.

PF 28-DEC-2000; 2000WO-EP013311.

PR 30-DEC-1999; 99EP-00126194.

PA (KLESE/) KLESEIEK K.

PI Kleeseiek K, Brinkmann T, Goetting C, Kuhn J;

DR WPI; 2001-441872/47.

PT UDP-xylose:proteoglycan core protein beta-D-xylosyltransferase and the
 nucleic acids that encode it, useful for preventing, diagnosing and
 treating sclerotic diseases and chronic inflammatory joint diseases.

PS Example 20; Page 29; 80pp; English.

CC The present sequence represents a PCR primer for a cDNA fragment encoding
 an isoform of UDP-xylose:proteoglycan core protein beta-D-
 xylosyltransferase (XT). The XT enzyme occurs in at least two isoforms
 (XT-I) and (XT-II). XT is involved in the biosynthesis of
 glycosaminoglycans. XT polypeptides and polynucleotides may be used in
 the production of an agent (inhibitors and antagonists of XT) for the
 treatment of sclerotic diseases and chronic inflammatory joint diseases,
 or as a diagnostic marker. The XT DNA may be used as a gene marker. Anti-XT
 antibodies are used as a diagnostic tool in a immunological assay for
 detection of a protein having XT activity

SQ Sequence 28 BP; 7 A; 2 C; 15 G; 4 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 4; Length 28;

Best Local Similarity 88.2%; Pred. No. 5.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCCCCCTCTGTGATA 18
 |||||
 DB 21 CCCCCCTCTGTGACAT 5

RESULT 6

ID ADL32573 standard; DNA; 22 BP.

AC ADL32573;

DT 03-JUN-2004 (first entry)

DE Human carbonic anhydrase II forward PCR primer SEQ ID NO:31.

KW detection; cancer; 8q22.3; chromosome 8; human; BDN; tumour suppressor;
 cell cycle modulator; DNA repair; DNA damage; nuclear targeting protein;
 progesterone receptor; cytosolic; gene therapy; squamous cell carcinoma;
 hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma;
 head and neck cancer; adenocarcinoma; squamous lung cancer;
 gastrointestinal cancer; renal cell cancer; bladder cancer;
 prostate cancer; non-squamous carcinoma; glioblastoma; medulloblastoma;
 carbonic anhydrase II; PCR; primer; ss.

OS Homo sapiens.
 OS Synthetic.

PN WO2004022750-A1.
XX 18-MAR-2004.
PD
XX 05-SEP-2003; 2b03WO-AU001164.
XX 05-SEP-2002; 2002AU-00951346.
XX 07-NOV-2002; 2002US-0425218P.
XX (GARV-) GARVAN INST MEDICAL RES.
PA
PI Watis C, Saunders D, Henderson M, Clancy J, Henshall S;
PI Sutherland R, O'Brien P;
PI
XX WPI; 2004-248472/23.
DR
XX Detecting a cancer cell in a subject sample, also related to cancer
FT treatments, comprises determining the level of nucleic acid that is
PT linked to map position 8q22.3 of the human genome or its expression
PT product.

XX Example 1; SEQ ID NO 31; 331pp; English.

XX The present invention describes a method for detecting a cancer cell in a
CC subject, which comprises determining the level of nucleic acid that is
CC linked to map position 8q22.3 of the human genome or its expression
CC product in a sample of the subject, where an elevated level of the
CC nucleic acid or polypeptide is indicative of cancer in the subject. Also
CC described: (1) a method for diagnosing a cancer or predicting recurrence
CC of a cancer in a subject comprising determining the level of mRNA or
CC protein encoded by a nucleic acid as described above; (2) the isolated
CC nucleic acid molecule for detecting cancer cell; (3) an isolated or
CC recombinant protein complex; (4) an antibody that binds to the protein
CC complex; (5) a kit for detecting or producing a protein complex
CC comprising an EDD polypeptide or a portion of an EDD polypeptide and a
CC second polypeptides selected from a protein having tumour suppressor
CC activity, a protein having cell cycle regulatory activity, a protein
CC associated with DNA repair or damage, a nuclear targeting protein, and a
CC progesterone receptor protein or its portion, where the portion of the
CC second polypeptide is sufficient to bind to the EDD polypeptide or the
CC portion of an EDD polypeptide; (6) methods for isolating the protein
CC complex; (7) a method for determining a predisposition for disease, or
CC disease state; (8) a method for determining a modulator of the activity,
CC formation or stability of an isolated or recombinant protein complex; (9)
CC a method for determining a modulator of the level of protein complex
CC formation; (10) a method for treating a condition associated with
CC elevated expression of EDD protein in a cell; (11) an antisense nucleic
CC acid, ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA; and
CC (12) a pharmaceutical composition comprising the antisense nucleic acid,
CC ribozyme, PNA, interfering RNA or siRNA. EDD has cytostatic activity, and
CC can be used in gene therapy. The methods and modulator are useful for
CC treating a condition associated with EDD over expression such as cancer,
CC e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer,
CC breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous
CC lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic
CC cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous
CC carcinoma, glioblastoma and medulloblastoma. The components and
CC composition are useful for reducing the expression of EDD in a cell to
CC inhibit cellular proliferation. The present sequence represents a PCR
CC primer for human carbonic anhydrase II, which is used in the
CC exemplification of the present invention.

XX Sequence 22 BP; 3 A; 10 C; 3 G; 6 T; 0 U; 0 Other;

XX Query Match 74.4%; Score 13.4; DB 12; Length 22;
XX Best Local Similarity 93.3%; Pred. No. 8.1e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCCTCTTGTGA 15
DB 5 CCCCCTCTTGTGA 19

RESULT 7

AD36420/c
ID ADC36420 standard; DNA; 20 BP.

XX AD36420;

DT 18-DEC-2003 (first entry)

XX Weed controller metabolism associated PCR primer SEQ ID NO:288.

XX Weed controller metabolism; weed; herbicide; herbicide-resistant plant;

XX agrochemical; seq; PCR; primer.

XX Synthetic.

PN WO2003040370-A1.

XX 15-MAY-2003.

XX 17-OCT-2002; 2002WO-JP010789.

XX 19-OCT-2001; 2001JP-00321307.

XX 07-JUN-2002; 2002JP-00167239.

XX (SDMO) SUMITOMO CHEM CO LTD.

PI Nakajima H, Mukumoto F, Takashi M;

PI WPI; 2003-523102/49.

XX Weed controller metabolism proteins deactivating porphyrinogen oxidase
PT (PPO)-inhibiting herbicides by N-demethylation and their genes, useful
PT e.g. in constructing new breeds of herbicide-resistant plants.

XX Disclosure: SEQ ID NO 288; 812pp; Japanese.

XX The invention relates to a novel DNA encoding a weed controller
CC metabolism protein. A protein of the invention has herbicide activity.

CC The proteins and their encoded genes are useful e.g. in constructing new
CC breeds of herbicide-resistant plants and also in developing various
CC agrochemicals. The present sequence is used in the exemplification of the
CC invention.

CC Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

XX Query Match 73.3%; Score 13.2; DB 10; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 1e+04;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCTCTTGTGATAC 18
DB 18 CCACCGTCCTCGATAC 1

XX RESULT 8
XX AD31445/c
XX ID AD31445 standard; DNA; 27 BP.

XX AD31445;

DT 26-FEB-2004 (first entry)

XX PCR primer used to amplify human c-erbB2 DNA SeqID 113.

XX human; PCR; seq; primer; MN/CA IX; MN; oncogene; carbonic anhydrase 9;

XX CA9; MN/CA9; carbonic anhydrase IX; CA IX; MN/G250; neoplastic tumour;

XX cytostatic; cancer; tumour therapy; anti-tumour vaccine.

XX Homo sapiens.

XX WO2003100029-A2.

XX 04-DEC-2003.

XX 22-FEB-2003; 2003WO-US005136.
PF XX
XX 23-MAY-2002; 2002US-0383068P.
PR XX
XX 05-DEC-2002; 2002US-0431499P.
XX
PA (FARB) BAYER CORP.
PA (VIBRO-) INST VIROLOGY.
XX
PI Pastorek J, Pastorekova S, Zalcovickova M, Zavada J, Ortova Gut M;
XX WPI; 2004-035136/03.
XX
PT New monoclonal antibody generated from MN/CA IX-deficient mice, where the
PT antibody binds specifically to human tumor-associated cell adhesion
PT protein MN/CA IX or polypeptide, useful for diagnosing, prognosing or
PT treating cancer.
XX
PS Example 11; SEQ ID NO 113; 156pp; English.
XX
CC This invention relates to a novel monoclonal antibody identified as the
CC MN/CA IX specific antibody prepared in knockout mice (CA IX deficient
CC mice). Specifically, this antibody is directed towards the MN gene, a
CC cellular oncogene known alternatively as carbonic anhydrase 9, CA9 or
CC MN/CA9, which encodes the MN protein that is also known as the MN/CA IX
CC isoenzyme, carbonic anhydrase IX, CA IX or the MN/G250 protein. The
CC present invention describes the generation of this monoclonal antibody,
CC and immunoreactive fragments thereof, which are directed against non-
CC immunodominant epitopes on the CA IX extracellular domain. As such, this
CC antibody can be useful diagnostically as a marker for preneoplastic/
CC neoplastic tumors, immunodetection methods and immunotargeting
CC approaches. Accordingly, compositions exhibit cytostatic activity and are
CC useful in the diagnosis, prognosis and treatment of various cancers
CC including breast, bladder or lung cancer, in tumor therapy and in anti-
CC tumor vaccination. This oligonucleotide sequence is an PCR primer used
CC to amplify DNA of a human breast tumor marker, in an exemplification of
CC the invention.
XX
SQ Sequence 27 BP; 6 A; 6 C; 10 G; 5 T; 0 U; 0 Other;
XX
Query Match 73.3%; Score 13.2; DB 12; Length 27;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 CCCCCCTCTCTGGAATAC 18
DB 19 CCCTCCTCATCTGGAAC 2
XX
RESULT 9
ADK41856/c
ID ADK41856 standard; DNA; 27 BP.
XX
AC ADK41856;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human MN gene-related PCR primer SegID109.
XX
XX carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
XX human; vertebrate; cytostatic; vaccine; gene therapy;
XX renal cell carcinoma; breast cancer; colorectal cancer; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2004005348-A1.
XX
XX 15-JAN-2004.
XX
XX 22-FEB-2003; 2003WO-US005137.
XX
XX 23-MAY-2002; 2002US-0383068P.
XX
XX 05-DEC-2002; 2002US-0431499P.
XX

XX (FARB) BAYER CORP.
PA (VIBRO-) INST VIROLOGY.
XX
XX Zavada J, Pastorekova S, Pastorek J, Zavadova Z;
XX WPI; 2004-083500/08.
XX
XX New soluble form of the carbonic anhydrase IX (CA IX) protein for
XX screening, diagnosing or prognosing diseases associated with abnormal
XX expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
XX colorectal cancer.
XX
PS Example 11; SEQ ID NO 113; 159pp; English.
XX
XX This invention relates to a novel soluble form of the carbonic anhydrase
XX IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
XX precancerous and/or cancerous cells of a vertebrate into a body fluid.
XX The invention may be useful for the development of compounds with a
XX cytostatic activity or a vaccine whilst the disclosed sequences may be
XX used for gene therapy. The protein and method are useful for screening,
XX diagnosing or prognosing diseases associated with abnormal expression of
XX carbonic anhydrase IX protein, such as precancerous and cancerous
XX diseases like renal cell carcinoma, breast cancer or colorectal cancer.
XX The monoclonal antibody may also be used for treating or preventing
XX precancerous and cancerous diseases. The present sequence is that of a
XX PCR primer which was used in the exemplification of the invention.
XX
SQ Sequence 27 BP; 6 A; 6 C; 10 G; 5 T; 0 U; 0 Other;
XX
Query Match 73.3%; Score 13.2; DB 12; Length 27;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 CCCCCCTCTCTGGAATAC 18
DB 19 CCCTCCTCATCTGGAAC 2
XX
RESULT 10
ADC36414
ID ADC36414 standard; DNA; 28 BP.
XX
AC ADC36414;
XX
XX 18-DEC-2003 (first entry)
XX
XX Weed controller metabolism associated PCR primer SEQ ID NO:282.
XX
XX weed controller metabolism; weed; herbicide; herbicide-resistant plant;
XX agrochemical; ss; PCR; primer.
XX
XX Synthetic.
XX
XX WO2003040370-A1.
XX
XX 15-MAY-2003.
XX
XX 17-OCT-2002; 2002WO-JP010789.
XX
XX 19-OCT-2001; 2001JP-00321307.
XX
XX 07-JUN-2002; 2002JP-00167239.
XX
XX (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Nakajima H, Mukumoto F, Takaiishi M;
XX WPI; 2003-523102/49.
XX
XX Weed controller metabolism proteins deactivating porphyrinogen oxidase
XX (PPO)-inhibiting herbicides by N-demethylation and their genes, useful
XX e.g. in constructing new breeds of herbicide-resistant plants.
XX
XX

PS Disclosure; SEQ ID NO 282; 812bp; Japanese.
XX
CC The invention relates to a novel DNA encoding a weed controller
CC metabolism protein. A protein of the invention has herbicide activity.
CC The proteins and their encoded genes are useful e.g. in constructing new
CC breeds of herbicide-resistant plants and also in developing various
CC agrochemicals. The present sequence is used in the exemplification of the
CC invention.
SQ Sequence 28 BP; 5 A; 11 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 73.3%; Score 13.2; DB 10; Length 28;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCCCCCTCTCTGGATAC 18
DB 11 CCACCGTCTCTGGATAC 28
RESULT 11
ACA54549/c
ID ACA54549 standard; DNA; 30 BP.
XX
AC ACA54549;
XX
XX 27-OCT-2003 (revised)
DT 19-JUN-2003 (first entry)
XX
XX Prokaryotic folA gene PCR primer #1.
XX
XX Antisense; ss; prokaryotic essential gene; cell proliferation;
KW drug design; primer; PCR.
XX
XX Archaea.
OS
XX WO200277183-A2.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 21-MAR-2002; 2002WO-US009107.
PF
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreysyh RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Example 21; Page 1574; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation; (7) the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is a PCR primer used
CC to amplify isolated DNA from an essential gene which, when overexpressed,
CC allows growth in the presence elevated antibiotic concentrations.
XX (Updated on 27-OCT-2003 to standardise OS field)
XX
SQ Sequence 30 BP; 11 A; 3 C; 10 G; 6 T; 0 U; 0 Other;
XX
Query Match 73.3%; Score 13.2; DB 8; Length 30;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCCCCCTCTCTGGATAC 18
DB 21 CCTCCTTCTCTGGATCC 4
RESULT 12
ABX13526/c
ID ABX13526 standard; DNA; 30 BP.
XX
XX ABX13526;
AC
XX
XX 04-JUN-2003 (first entry)
DT
XX
XX
XX *S. aureus* folA PCR primer SEQ ID 15798.
DE
XX
XX Cellular proliferation; inhibitor; target; primer; PCR; folA;
KW trimethoprim; ss.
XX
XX
XX *Staphylococcus aureus*.
OS
XX
XX WO200286097-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 08-FEB-2002; 2002WO-US003987.
PF
XX
XX 09-FEB-2001; 2001US-0267636P.
PR
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Carr GJ, Xu HH, Foulkes GJ, Zamudio C, Haselbeck R, Ohlsen KL;
PI Zyskind JW, Wall D, Trawick JD, Yamamoto RT, Roemer T, Jiang B,
PI Boone C, Bussey H;
XX
XX WPI; 2003-093128/08.
DR
XX
XX Identifying the target of a compound which inhibits cellular
PT proliferation, comprises contacting a culture of strains that overexpress
PT or underexpress a gene product with the above compound, and identifying
PT the gene product.
XX
XX Example 16; Page 315; 640pp; English.
XX
XX This invention describes a novel method for identifying gene products on
CC which compounds inhibiting proliferation of an organism act. The method
CC comprises obtaining a culture of strains overexpressing a different
CC product for proliferation of the organism, contacting the culture with a
CC compound to inhibit proliferation of strains that do not overexpress the

CC product and identifying the product overexpressed in a strain that
CC proliferated more rapidly. The method is useful in identifying the target
CC of a compound which reduces the activity or level of gene products
CC required for cellular proliferation. The method may also be used for
CC identifying the therapeutic compounds that act on the novel targets. This
CC sequence represents a PCR primer used to amplify the *Staphylococcus*
CC *aureus* *folA* gene which is inhibited by trimethoprim

XX
SQ Sequence 30 BP; 11 A; 3 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 8; Length 30;

Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCCCTTTCTTGAT 18
DB 21 CCTCCTTCTTGATCC 4

RESULT 13

ADH30251
ID ADH30251 standard; DNA; 17 BP.

AC ADH30251;

DT 11-MAR-2004 (first entry)

DE Human monocyte-macrophage cell surface apob48 receptor primer #5.

XX
XX antilipemic; gene therapy;

KW monocyte-macrophage cell surface apob48 receptor; apob48r;
KW pattern B phenotype; familial combined hyperlipidaemia;

KM hypercholesterolaemia; hypertriglyceridaemia;
KM low plasma high-density lipoprotein level; human; primer; ss.

XX
XX Homo sapiens.

OS
XX US2003208060-A1.

PN
XX 06-NOV-2003.

PD
XX 12-JUN-2003; 2003US-00459876.

PF
XX 06-AUG-1998; 98US-00130242.

PR
XX 31-MAY-2000; 2000US-00583610.

XX
XX (GIAN/) GIANTURCO S H.
XX (BRAD/) BRADLEY W A.

PI
XX Gianturco SH, Bradley WA;

DR
XX WPI; 2003-864799/80.

XX
XX New isolated DNA molecule encoding a monocyte-macrophage cell surface
XX apob48 receptor protein (apob48r), useful in preparing a composition for
XX treating e.g., familial or non-familial hypercholesterolaemia.

XX
XX Example 23; SEQ ID NO 17; 77pp; English.

XX
XX The invention describes a new isolated DNA molecule, encoding a monocyte-
XX macrophage cell surface apob48 receptor protein (apob48r) comprising a
XX fully defined 1088 amino acid sequence. The DNA molecule is useful in
XX preparing a composition for treating pattern B phenotype, familial
XX combined hyperlipidaemia, familial or non-familial hypercholesterolaemia,
XX hypertriglyceridaemia or low plasma high-density lipoprotein levels. This
XX sequence represents a primer used in the isolation of human monocyte-
XX macrophage cell surface apob48 receptor DNA.

XX
SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 10; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCCTTTCTTGAT 16
DB 1 CCAGCCTTCTTGAT 16

RESULT 14

AD000840
ID AD000840 standard; DNA; 17 BP.

AC AD000840;

DT 12-AUG-2004 (first entry)

DE Human monocyte-macrophage cell surface apob48r cDNA PCR primer #6.

XX
XX Human; monocyte-macrophage cell surface apolipoprotein B 48 receptor;
KW apolipoprotein B 48 receptor; apob48r; PCR; ss; monocyte; macrophage;

KW reticuloendothelial cell; monocyte adhesion; cardiovascular disease;
KW apob-mediated cellular uptake; plasma chylomicron;

KM hypertriglyceridaemia; triglyceride-rich lipoprotein;
KW Apob independent pathway; lipoprotein lipase independent pathway;

KM heparin sulfate proteoglycan independent pathway; foam cell formation;
KM hypertriglyceridaemia; primer.

XX
XX Homo sapiens.

OS
XX US6740735-B1.

PN
XX 25-MAY-2004.

PD
XX 31-MAY-2000; 2000US-00583610.

PF
XX 06-AUG-1998; 98US-00130242.

PR
XX (GIAN/) GIANTURCO S H.
XX (BRAD/) BRADLEY W A.

PI
XX Gianturco SH, Bradley WA;

DR
XX WPI; 2004-387250/36.

XX
XX New isolated monocyte-macrophage cell surface apob48 receptor protein,
XX useful for cell-specific delivery of therapeutic compounds to human
XX monocytes or macrophages, or for evaluating an individual at risk for
XX cardiovascular disease.

XX
XX Example 23; SEQ ID NO 17; 72pp; English.

XX
XX The invention relates to the human monocyte-macrophage cell surface
XX apolipoprotein B 48 receptor (apob48r) protein and the nucleic acid
XX encoding it. The invention also relates to a method of cell-specific
XX delivery of therapeutic compounds to human monocytes, macrophages or
XX other reticuloendothelial cells that express the receptor, a method of
XX inhibiting foam cell formation and increased monocyte adhesion to
XX endothelial cells and a method of evaluating an individual at risk of a
XX cardiovascular disease. The monocyte-macrophage cell surface apob48
XX receptor protein is useful in the apob-mediated cellular uptake of plasma
XX chylomicrons and remnants and hypertriglyceridaemic triglyceride-rich
XX lipoproteins in an Apob independent pathway, a lipoprotein lipase
XX independent pathway or a heparin sulfate proteoglycan independent
XX pathway. It is also useful for the cell-specific delivery of therapeutic
XX compounds to human monocytes, macrophages or other reticuloendothelial
XX cells that express the receptor, for inhibiting foam cell formation and
XX increased monocyte adhesion to endothelial cells and for evaluating an
XX individual at risk of a cardiovascular disease such as
XX hypertriglyceridaemia. This sequence represents a PCR primer used in
XX cloning of cDNA encoding the apob48r protein of the invention.

XX
SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 12; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.6e+04;

	Matches	14, Conservative	0, Mismatches	2, Indels	0, Gaps
QY	1	CCCCCTTTCTTGAT	16		
DB	1	CCAGCCTTTCTTGAT	16		

Db 16 CCTCCTCTGCTGGAT 1

Search completed: April 7, 2006, 08:51:15
Job time : 360.081 secs

RESULT 15

ADN08161 standard; DNA; 18 BP.

ADN08161 standard; DNA; 18 BP.

ADN08161;

ADN08161;

DT 17-JUN-2004 (first entry)

DE Human S9-RNA RT-PCR primer #2.

Human: **aa**: PCB: endocrine gland vascular endothelial growth factor;
xx

KM EG-VEGF; EG-VEGF receptor; endometrial disease; uterine receptivity;
KM endometriosis; endometrial carcinoma; dysfunctional bleeding;

KW gene therapy; primer; RT-PCR; reverse transcriptase PCR; S9-RNA.

Homo sapiens.

XX
PN DE10229379-A1

DE10229379-A1

XX 39-TAN-2004
PD

29-TAN-2004

333

XX	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82</
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	------

26-JUN-2002; 2002DE-010293/9-
PK
XX

PA (SCHD) SCHERING AG.
XX

(SCHD) SCHERING AG.

PI Haendler B, Hees-Stumpf H, Schmidt A;

WPI; 2004-134408/14.

WPI; 2004-134408/14.

XX	PT	Treatment and prevention of endometrial disease, e.g. endometriosis or

PT carcinoma, by inhibiting endocrine gland and vascular endothelial growth factor. *Allopathy*.

carcinoma, by inhibiting factor. A110.0 MAGNOSTE.

XX Bureau of the Peace, E. 13th, New York

11 - Bureau of Census

The invention relates to a composition that contains, as active agent, an endocrine gland vascular endothelial growth factor (EG-VEGF) nucleic acid, polypeptide or antisense nucleic acid, antibody against EG-VEGF or its receptor (EG-VEGF-R), or EG-VEGF-R antisense nucleic acid, is useful for the treatment or prevention of endometrial diseases. Also included are a method for detecting uterine receptivity (by determining the amount of EG-VEGF polypeptide and/or nucleic acid, using the new composition) or a test system for identifying antagonists of EG-VEGF-R. Also disclosed as new is a splice variant of the human GPR73A receptor. It contains an additional exon which includes a stop codon, so produces a truncated protein that can not mediate signal transduction, i.e. it functions as a dominant-negative inhibitor. The composition is used to treat endometriosis, endometrial carcinoma or dysfunctional bleeding, e.g. by gene therapy, to diagnose endometriosis or endometrial carcinoma and to detect uterine receptivity (especially to determine the best time for implantation of eggs fertilised in vitro). Also the test system that comprises cells that express the EG-VEGF receptor is used to screen for receptor antagonists, potentially useful for treating endometriosis. The present sequence is a human 59-nucleotide RT-PCR (reverse transcriptase PCR) primer used in the isolation of the EG-VEGF cDNA.

Sequence 18 BP; 6 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Sequence 18 BP; 6 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match	71.1%;	Score 12.8;	DB 12;	Length 18;
-------------	--------	-------------	--------	------------

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Best Local Similarity  87.58;  E-Val: NO: 1.00E-03;
Matches  14;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

```

1 CCCCCCTCTCTGGAT 16

Figure 1

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: EP 1502948-A 8 02-FEB-2005;
Aguaria Inc. (US)

FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Probe"

ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
| | | | | | | | | | | | | | | | | | |
1 TCCCCCACTCGAAGATACG 19

RESULT 3
AX316099
LOCUS AX316099 19 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 8 from Patent WO0190312.
AX316099
VERSION AX316099.1 GI:17899290
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hovanec, T.A. and Burrell, P.C.
TITLE Ammonia-oxidizing bacteria
JOURNAL Patent: WO 0190312-A 8 29-NOV-2001;
AQUARIA, INC. (US)

FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
| | | | | | | | | | | | | | | | | | |
1 TCCCCCACTCGAAGATACG 19

RESULT 4
AF134441/c
LOCUS AF134441 428 bp rRNA linear ENV 11-MAY-2004
DEFINITION Uncultured beta proteobacterium b4 16S ribosomal RNA, partial
sequence.
ACCESSION AF134441
VERSION AF134441.1 GI:4836726
KEYWORDS ENV.
SOURCE uncultured beta proteobacterium b4
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; environmental samples.
1 (bases 1 to 428)
REFERENCE Whitby, C.B., Saunders, J.R., Rodriguez, J., Pickup, R.W. and
AUTHORS McCarthy, A.
TITLE Phylogenetic differentiation of two closely related Nitrosomonas
 spp. That inhabit different sediment environments in an

JOURNAL Appl. Environ. Microbiol. 65 (11), 4855-4862 (1999)
PUBMED 10543796
REFERENCE 2 (bases 1 to 428)
AUTHORS Whitby, C.W., Saunders, J.R., Rodriguez, J., Pickup, R.W. and
McCarthy, A.J.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1999) School of Biological Sciences, University
of Liverpool, Crown Street, Liverpool, Merseyside L69 7ZB, UK

FEATURES
source
1. .428
/organism="uncultured beta proteobacterium b4"
/mol_type="rRNA"
/db_xref="taxon:93622"
/chromosome="1"
/clone="b4"
/environmental sample
/note="similar to Becherichia coli locus UBd4"
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 3; Length 428;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
| | | | | | | | | | | | | | | | | | |
63 TCCCCCACTCGAAGATACG 45

RESULT 5
AF134442/c
LOCUS AF134442 455 bp rRNA linear ENV 11-MAY-2004
DEFINITION Uncultured beta proteobacterium b5 16S ribosomal RNA, partial
sequence.
ACCESSION AF134442
VERSION AF134442.1 GI:4836727
KEYWORDS ENV.
SOURCE uncultured beta proteobacterium b5
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; environmental samples.
1 (bases 1 to 455)
REFERENCE Whitby, C.B., Saunders, J.R., Rodriguez, J., Pickup, R.W. and
AUTHORS McCarthy, A.
TITLE Phylogenetic differentiation of two closely related Nitrosomonas
 spp. That inhabit different sediment environments in an
oligotrophic freshwater lake
JOURNAL Appl. Environ. Microbiol. 65 (11), 4855-4862 (1999)
PUBMED 10543796
REFERENCE 2 (bases 1 to 455)
AUTHORS Whitby, C.W., Saunders, J.R., Rodriguez, J., Pickup, R.W. and
McCarthy, A.J.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1999) School of Biological Sciences, University
of Liverpool, Crown Street, Liverpool, Merseyside L69 7ZB, UK

FEATURES
source
1. .455
/organism="uncultured beta proteobacterium b5"
/mol_type="rRNA"
/db_xref="taxon:93626"
/chromosome="1"
/clone="b5"
/environmental sample
/note="similar to Becherichia coli locus UBd4"
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 3; Length 455;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
| | | | |
Db 28 TCCCCCACTCGAAGATACG 10

RESULT 6
LOCUS AY921481
DEFINITION Uncultured bacterium clone AF5 16S ribosomal RNA gene, partial sequence.
ACCESSION AY921481 GI:60327520
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 493)
AUTHORS Ka, J.-O., Jung, M.-K., Kim, M.-S. and Ahn, J.-H.
TITLE Changes in bacterial community in rice field soils
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 493)
AUTHORS Ka, J.-O., Jung, M.-K., Kim, M.-S. and Ahn, J.-H.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2005) School of Applied Biology and Chemistry, Seoul National University, San 56-1 Sillindong Kwanakgu, Seoul 151-921, Korea

FEATURES
source
1..493
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/db_xref="taxon:77133"
/clone="AF5"
/environmental_sample
complement(<1..>493)
/product="16S ribosomal RNA"

ORIGIN
rRNA
Query Match 100.0%; Score 19; DB 3; Length 493;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
| | | | |
Db 365 TCCCCCACTCGAAGATACG 383

RESULT 7
LOCUS AF408634/c
DEFINITION Nitrosospirota multiformis strain 24C 16S ribosomal RNA gene, partial sequence.
ACCESSION AF408634 GI:16139825
KEYWORDS Nitrosospirota multiformis
SOURCE Nitrosospirota multiformis
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosospirota.
REFERENCE 1 (bases 1 to 983)
AUTHORS Norton, J.M., Alzerreca, J.J., Suwa, Y. and Klotz, M.G.
TITLE Diversity of the amo operon in autotrophic ammonia-oxidizing bacteria
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 983)
AUTHORS Norton, J.M. and Klotz, M.G.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2001) Plant, Soils and Biometeorology, Utah State University, 4820 Old Main Hill, Logan, UT 84322, USA

FEATURES
source
1..983
/organism="Nitrosospirota multiformis"

ORIGIN
rRNA
Query Match 100.0%; Score 19; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
| | | | |
Db 74 TCCCCCACTCGAAGATACG 56

RESULT 8
LOCUS NSP298724/c
DEFINITION Nitrosospirota sp. 24C partial 16S rRNA gene, isolate 24C.
ACCESSION AJ298724 GI:117932725
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Nitrosospirota sp. 24C
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosospirota.
REFERENCE 1
AUTHORS Aakra, A., Utaker, J.B., Pommerening-Roser, A., Koops, H.P. and Nes, I.P.
TITLE Detailed phylogeny of ammonia-oxidizing bacteria determined by rDNA sequences and DNA homology values
JOURNAL Int. J. Syst. Evol. Microbiol. 51 (Pt 6), 2021-2030 (2001)
REFERENCE 2 (bases 1 to 1207)
AUTHORS Aakra, A.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-2000) Aakra A., Laboratory of Microbial Gene Technology, Agricultural University of Norway, P.O. Box 5051, N-1432 Aas, NORWAY

FEATURES
source
1..1207
/organism="Nitrosospirota sp. 24C"
/mol_type="genomic DNA"
/isolate="24C"
/db_xref="taxon:136540"
/country="USA:Minnesota"
1..1207
/gene="16S rRNA"
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ORIGIN
rRNA
Query Match 100.0%; Score 19; DB 1; Length 1207;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
| | | | |
Db 23 TCCCCCACTCGAAGATACG 5

RESULT 9
LOCUS NSAP16S/c
DEFINITION Nitrosospirota sp. 16S rRNA gene, isolate AF.
ACCESSION X84658 GI:1236774
KEYWORDS 16S ribosomal RNA.
SOURCE Nitrosospirota sp.
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Nitrosomonadaceae; Nitrospira.
Utaker, J.B., Bakken, L., Jiang, Q.Q. and Nes, I.F.
Phylogenetic analysis of seven new isolates of the highly related ammonia-oxidizing bacteria based on 16S rRNA gene sequencing
Syst. Appl. Microbiol. 18, 549-559 (1995)
2 (bases 1 to 1368)
Utaker, J.B.
Direct Submission
Submitted (09-FEB-1995) J.B. Utaker, Agricultural University of Norway, Lab of Microbial Gene Technology, PO Box 5051, 1432 Aas
NLH, NORWAY

FEATURES
Source
Location/Qualifiers
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/mol_type="genomic DNA"
/isolate="Af"
/db_xref="taxon:38080"
<1..>1368
/product="16S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 19; DB 1; Length 1368;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
|||||
Db 90 TCCCCCACTCGAAGATACG 72

RESULT 10
NTV16SRNA/c
LOCUS NTV16SRNA 1378 bp DNA linear BCT 12-OCT-1993
DEFINITION Nitrosovibrio tenuis 16S ribosomal RNA (16S rRNA) gene sequence.
ACCESSION M96404
VERSION M96404.1 GI:150439
KEYWORDS 16S ribosomal RNA.
SOURCE Nitrosovibrio tenuis
ORGANISM Nitrosovibrio tenuis
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosovibrio.
1 (bases 1 to 1378)
Head, I.M., Hiorns, W.D., Embley, T.M., McCarthy, A.J. and
Saunders, J.R.
The phylogeny of autotrophic ammonia-oxidizing bacteria as
determined by analysis of 16S ribosomal RNA gene sequences
J. Gen. Microbiol. 139 (Pt 6), 1147-1153 (1993)
7689633
COMMENT Original source text: Nitrosovibrio tenuis (strain Nv1) DNA.
FEATURES
Source
Location/Qualifiers
1..1378
/organism="Nitrosovibrio tenuis"
/mol_type="unassigned DNA"
/db_xref="taxon:1233"

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Query Match 100.0%; Score 19; DB 1; Length 1378;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
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Db 124 TCCCCCACTCGAAGATACG 106

RESULT 11
NS16SAV/c
LOCUS NS16SAV 1388 bp DNA linear BCT 19-DEC-2002
DEFINITION Nitrospira sp. NPAV partial 16S rRNA gene, strain NPAV.
ACCESSION Y10127
VERSION Y10127.2 GI:27262953
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Nitrospira sp. NPAV
Nitrospira sp. NPAV
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrospira.
1
McCaig, A.E., Embley, T.M. and Prosser, J.I.
Molecular analysis of enrichment cultures of marine ammonia
oxidisers
FEMS Microbiol. Lett. 120 (3), 363-367 (1994)
8076810
2
Prosser, J., Freitag, T. and Smith, Z.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Unpublished
3
McCaig, A.E.
Direct Submission
Submitted (18-DEC-1996) A.E. McCaig, Institute of Medical Sciences,
Molecular and Cell Biology, University of Aberdeen, Foresterhill,
Aberdeen, AB25 2ZD, UK
revised by [4]
4 (bases 1 to 1388)
McCaig, A.E.
Direct Submission
Submitted (08-NOV-2002) A.E. McCaig, Institute of Medical Sciences,
Molecular and Cell Biology, University of Aberdeen, Foresterhill,
Aberdeen, AB25 2ZD, UK
On Dec 19, 2002 this sequence version replaced gi.1771383.

COMMENT
FEATURES
Source
Location/Qualifiers
1..1388
/organism="Nitrospira sp. NPAV"
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/strain="NPAV"
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1..1236
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ORIGIN
Query Match 100.0%; Score 19; DB 1; Length 1388;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCCCACTCGAAGATACG 19
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Db 57 TCCCCCACTCGAAGATACG 39

RESULT 12
NTV16SRNA/c
LOCUS NTV16SRNA 1435 bp DNA linear BCT 12-OCT-1993
DEFINITION Nitrosovibrio tenuis 16S ribosomal RNA (16S rRNA) gene sequence.
ACCESSION M96397
VERSION M96397.1 GI:150441
KEYWORDS 16S ribosomal RNA.
SOURCE Nitrosovibrio tenuis
ORGANISM Nitrosovibrio tenuis
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosovibrio.
1 (bases 1 to 1435)
Head, I.M., Hiorns, W.D., Embley, T.M., McCarthy, A.J. and
Saunders, J.R.
The phylogeny of autotrophic ammonia-oxidizing bacteria as
determined by analysis of 16S ribosomal RNA gene sequences
J. Gen. Microbiol. 139 (Pt 6), 1147-1153 (1993)
7689633
COMMENT Original source text: Nitrosovibrio tenuis (strain C-141) DNA.
FEATURES
Source
Location/Qualifiers
1..1435
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/mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:1233"

Query Match 100.0%; Score 19; DB 1; Length 1435;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
135 TCCCCCACTCGAAGATACG 117

RESULT 13
AP386755/c 1469 bp DNA linear ENV 10-MAY-2004
LOCUS Nitrosospira sp. R5C20 16S ribosomal RNA gene, partial sequence.
ACCESSION AP386755
VERSION AP386755.1 GI:17864832
KEYWORDS ENV.
SOURCE Nitrosospira sp. R5C20
ORGANISM Nitrosospira sp. R5C20
REFERENCE Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria
JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
PUBMED 11722936
2 (bases 1 to 1469)
Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr, Moorpark, CA 93021, USA
Location/Qualifiers
FEATURES
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1. 1469
/organism="Nitrosospira sp. R5C20"
/mol_type="genomic DNA"
/isolation_source="ammonia-oxidizing bacteria isolated from freshwater aquaria enrichments"
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/clone="R5C20"
/environmental_sample
<1. >1469
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 3; Length 1469;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
133 TCCCCCACTCGAAGATACG 115

RESULT 14
AF386754/c 1486 bp DNA linear ENV 10-MAY-2004
LOCUS Nitrosospira sp. B16c46 16S ribosomal RNA gene, partial sequence.
ACCESSION AF386754
VERSION AF386754.1 GI:17864831
KEYWORDS ENV.
SOURCE Nitrosospira sp. B16c46
ORGANISM Nitrosospira sp. B16c46
REFERENCE Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria
JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
PUBMED 11722936

REFERENCE 2 (bases 1 to 1486)
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr, Moorpark, CA 93021, USA
Location/Qualifiers
FEATURES
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1. 1486
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/mol_type="genomic DNA"
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/db_xref="taxon:180513"
/clone="B16c46"
/environmental_sample
<1. >1486
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 3; Length 1486;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCCCCACTCGAAGATACG 19
131 TCCCCCACTCGAAGATACG 113

RESULT 15
AY856079/c 1495 bp DNA linear BCT 12-JAN-2005
LOCUS Nitrosospira sp. En13 16S ribosomal RNA gene, partial sequence.
ACCESSION AY856079
VERSION AY856079.1 GI:57232110
KEYWORDS ENV.
SOURCE Nitrosospira sp. En13
ORGANISM Nitrosospira sp. En13
REFERENCE Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria
JOURNAL Submitted (14-DEC-2004) School of Biological Sciences, University of Aberdeen, Cruickshank Building, St Machar Drive, Aberdeen AB24 3UU, U.K.
Location/Qualifiers
FEATURES
source
1. 1495
/organism="Nitrosospira sp. En13"
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/db_xref="taxon:308023"
<1. >1495
/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 19; DB 1; Length 1495;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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116 TCCCCCACTCGAAGATACG 98

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Matches    14; Conservative   0; Mismatches    0; Indels    0; Gaps    0;

QY          2 CCCCTCTTCTGGA 15
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Db           20 CCCCTCTTCTGGA 7

RESULT 2
US-11-121-849-112898
; Sequence 112898, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
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;; PRIOR FILING DATE: 2004-05-03
;; NUMBER OF SEQ ID NOS: 673904
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 112898
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-121-849-112898

Query Match 77.8%; Score 14; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCCCTCTGTGATA 17
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DB 6 CCCCTCTGTGATA 19

RESULT 3
US-11-101-244-1230837
;; Sequence 1230837, Application US/11101244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 1349905
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 1230837
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-1230837

Query Match 72.2%; Score 13; DB 12; Length 19;
Best Local Similarity 61.5%; Pred. No. 8e+02; 0; Indels 0; Gaps 0;
Matches 8; Conservative 5; Mismatches 0;

QY 6 CTCCTCTGTGATAC 18
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DB 4 CUCUCUCUGAUAAC 16

RESULT 4
US-11-083-784-1230837
;; Sequence 1230837, Application US/11083784
;; Publication No. US20050245475A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 1349905
;; CURRENT APPLICATION NUMBER: US/11/083,784
;; CURRENT FILING DATE: 2005-03-18
;; PRIOR APPLICATION NUMBER: US/10/714,333
;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10

;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 1230837
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-1230837

Query Match 72.2%; Score 13; DB 13; Length 19;
Best Local Similarity 61.5%; Pred. No. 8e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCCTCTGTGATAC 18
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DB 4 CUCUCUCUGAUAAC 16

RESULT 5
US-10-310-914A-224598
;; Sequence 224598, Application US/10310914A
;; Publication No. US20060003322A1
;; GENERAL INFORMATION:
;; APPLICANT: Benwich, Isaac
;; APPLICANT: Shlier, Kuzat
;; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;; FILE REFERENCE: 06087,0200,CPUS01
;; CURRENT APPLICATION NUMBER: US/10/310,914A
;; CURRENT FILING DATE: 2002-12-06
;; NUMBER OF SEQ ID NOS: 1388402
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 224598
;; LENGTH: 23
;; TYPE: RNA
;; ORGANISM: Human
US-10-310-914A-224598

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Best Local Similarity 69.2%; Pred. No. 8e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCCTCTGTGGA 15
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DB 9 CCCUCUCUGAUAAC 21

RESULT 6
US-10-934-048A-68320
;; Sequence 68320, Application US/10934048A
;; Publication No. US2006005170A1
;; GENERAL INFORMATION:
;; APPLICANT: Tanya Makeev
;; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
;; FILE REFERENCE: 3699
;; CURRENT APPLICATION NUMBER: US/10/934,048A
;; CURRENT FILING DATE: 2004-09-03
;; NUMBER OF SEQ ID NOS: 120855
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 68320
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: S. pombe
US-10-934-048A-68320

Query Match 72.2%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCCTCTGTGATAC 18
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DB 4 CTCCTCTGTGATAC 16

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RESULT 7
US-11-121-849-325988
; Sequence 325988, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIORITY FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 325988
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-325988

Query Match      72.2%; Score 13; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 CCCCTCTTCTGGA 15
Db      9 CCCCTCTTCTGGA 21

RESULT 8
US-10-310-914A-224589
; Sequence 224589, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224589
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-224589

Query Match      72.2%; Score 13; DB 8; Length 27;
Best Local Similarity 69.2%; Pred. No. 8e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY      3 CCCCTCTTCTGGA 15
Db      8 CCCCTCTTCTGGA 20

RESULT 9
US-10-310-914A-439308/c
; Sequence 439308, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
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; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-439308

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Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 CCCCTCTTCTGG 14
Db      12 CCCCTCTTCTGG 1

RESULT 10
US-10-310-914A-552172/c
; Sequence 552172, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 552172
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-552172

Query Match      66.7%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 CCCCTCTTCTCT 12
Db      18 CCCCTCTTCTCT 7

RESULT 11
US-10-310-914A-1226662/c
; Sequence 1226662, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
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; SEQ ID NO 1226662
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1226662

Query Match      66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 CCCCTCTTCTGG 14
Db      17 CCCCTCTTCTGG 6
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RESULT 12
US-11-101-244-603439/c
; Sequence 603439, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 603439
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-603439

Query Match 66.7%; Score 12; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCTCTGGATAC 18
Db 18 TCTCTGGATAC 7

RESULT 13
US-11-101-244-815438/c
; Sequence 815438, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 815438
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-815438

Query Match 66.7%; Score 12; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCTCTGGATAC 18
Db 18 TCTCTGGATAC 7

RESULT 14
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; Sequence 815537, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 815537
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-815537

Query Match 66.7%; Score 12; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCTCTGGATAC 18
Db 18 TCTCTGGATAC 7

RESULT 15
US-11-101-244-817168/c
; Sequence 817168, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 817168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-817168

Query Match 66.7%; Score 12; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCTCTGGATAC 18
Db 18 TCTCTGGATAC 7

Mon Apr 10 08:45:41 2006

us-10-659-980a-5.011g_sz30.rmpbn

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Perfect score: 18
Sequence: 1 cccccctctctgataac 18

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Published Applications NA Main:*

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18	100.0	18	US-10-659-948A-5	Sequence 5, Appl1
2	18	100.0	18	US-10-659-980A-5	Sequence 5, Appl1
3	18	100.0	18	US-10-659-983A-5	Sequence 5, Appl1
4	13	72.2	25	US-10-719-956-117959	Sequence 117959,
5	13	72.2	25	US-10-719-956-193006	Sequence 193006,
6	13	72.2	25	US-10-719-956-470164	Sequence 470164,
7	13	72.2	25	US-10-719-956-511003	Sequence 511003,
8	13	72.2	25	US-10-719-956-558629	Sequence 558629,
9	13	72.2	25	US-10-719-956-611802	Sequence 611802,
10	13	72.2	25	US-10-719-956-616050	Sequence 616050,
11	13	72.2	25	US-10-719-956-616050	Sequence 616050,
12	13	72.2	25	US-10-719-956-616050	Sequence 616050,
13	13	72.2	25	US-10-719-956-616050	Sequence 616050,
14	13	72.2	25	US-10-719-956-616050	Sequence 616050,
15	13	72.2	25	US-10-719-956-616050	Sequence 616050,
16	13	72.2	25	US-10-719-956-616050	Sequence 616050,
17	13	72.2	25	US-10-719-956-616050	Sequence 616050,
18	13	72.2	25	US-10-719-956-616050	Sequence 616050,
19	13	72.2	25	US-10-719-956-616050	Sequence 616050,
20	13	72.2	25	US-10-719-956-616050	Sequence 616050,
21	13	72.2	25	US-10-719-956-616050	Sequence 616050,
22	13	72.2	25	US-10-719-956-616050	Sequence 616050,
23	13	72.2	25	US-10-719-956-616050	Sequence 616050,

C 24	12	66.7	25	5	US-10-215-112-6677	Sequence 6677, Ap
C 25	12	66.7	25	6	US-10-122-114-1	Sequence 1, Appl1
C 26	12	66.7	25	7	US-10-719-956-5244	Sequence 5244, Ap
C 27	12	66.7	25	7	US-10-719-956-60519	Sequence 60519, A
C 28	12	66.7	25	7	US-10-719-956-135610	Sequence 135610,
C 29	12	66.7	25	7	US-10-719-956-141295	Sequence 141295,
C 30	12	66.7	25	7	US-10-719-956-165636	Sequence 165636,
C 31	12	66.7	25	7	US-10-719-956-169435	Sequence 169435,
C 32	12	66.7	25	7	US-10-719-956-170455	Sequence 170455,
C 33	12	66.7	25	7	US-10-719-956-170701	Sequence 170701,
C 34	12	66.7	25	7	US-10-719-956-170701	Sequence 170701,
C 35	12	66.7	25	7	US-10-719-956-170701	Sequence 170701,
C 36	12	66.7	25	7	US-10-719-956-170701	Sequence 170701,
C 37	12	66.7	25	7	US-10-719-956-613937	Sequence 613937,
C 38	12	66.7	25	7	US-10-719-956-620295	Sequence 620295,
C 39	12	66.7	25	7	US-10-719-956-676929	Sequence 676929,
C 40	12	66.7	25	8	US-10-719-956-226025	Sequence 226025,
C 41	12	66.7	25	8	US-10-719-956-242303	Sequence 242303,
C 42	12	66.7	25	8	US-10-719-956-242303	Sequence 242303,
C 43	12	66.7	25	8	US-10-719-956-290325	Sequence 290325,
C 44	12	66.7	25	8	US-10-719-956-307739	Sequence 307739,
C 45	12	66.7	25	8	US-10-719-956-416880	Sequence 416880,

ALIGNMENTS

RESULT 1
US-10-659-948A-5
Sequence 5, Application US/10659948A
Publication No. US20040101946A1
GENERAL INFORMATION:
APPLICANT: Hovaneec, Timothy A
TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-294309
CURRENT APPLICATION NUMBER: US/10/659, 948A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US 09/573, 684
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/386, 217
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386, 218
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386, 219
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5:
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Oligonucleotide Probe
US-10-659-948A-5
Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 CCCCCCTCTCTGATAC 18
1 CCCCCCTCTCTGATAC 18
RESULT 2
US-10-659-980A-5
Sequence 5, Application US/10659980A
Publication No. US20040106133A1
GENERAL INFORMATION:
APPLICANT: Hovaneec, Timothy A
TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-284761
CURRENT APPLICATION NUMBER: US/10/659, 980A

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; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Probe
US-10-659-980A-5

Query Match      100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCCCCCTCTGTGATAC 18
DB      1  CCCCCCTCTGTGATAC 18

RESULT 3
US-10-659-983A-5
; Sequence 5, Application US/10659983A
; Publication No. US2004015731A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-28479
; CURRENT APPLICATION NUMBER: US/10/659,983A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Probe
US-10-659-983A-5

Query Match      100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCCCCCTCTGTGATAC 18
DB      1  CCCCCCTCTGTGATAC 18

RESULT 4
US-10-719-956-117959/C
; Sequence 117959, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; OTHER INFORMATION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
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; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 117959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-117959

Query Match      72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  CTCTCTGTGATAC 18
DB      19 CTCTCTGTGATAC 7

RESULT 5
US-10-719-956-193006
; Sequence 193006, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 193006
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-193006

Query Match      72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  CCCTCTTCTGGAT 16
DB      4  CCCTCTTCTGGAT 16

RESULT 6
US-10-719-956-470164
; Sequence 470164, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 470164
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-470164

Query Match      72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 5 CCTCTCTGGATA 17
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Db 13 CCTCTCTGGATA 25

RESULT 7
US-10-719-956-511003
; Sequence 511003, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 511003
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-511003

Query Match 72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCTCTCTGGAT 16
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Db 10 CCTCTCTGGAT 22

RESULT 8
US-10-719-956-558629
; Sequence 558629, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 558629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-558629

Query Match 72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCTCTCTGGAT 16
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Db 7 CCTCTCTGGAT 19

RESULT 9
US-10-719-956-611802
; Sequence 611802, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 611802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-611802

Query Match 72.2%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CCTCTCTGGA 15
| | | | | | | | | | | | | | | | | |
Db 6 CCTCTCTGGA 18

RESULT 10
US-10-719-900-316050
; Sequence 316050, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 316050
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-316050

Query Match 72.2%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CCTCTCTGGATA 17
| | | | | | | | | | | | | | | | | |
Db 4 CCTCTCTGGATA 16

RESULT 11
US-10-719-900-574815
; Sequence 574815, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 574815
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-574815

Query Match 72.2%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCCTCTTGATAC 18
| | | | | | | | | |
| | | | | | | | | |
Db 7 CTCCTCTTGATAC 19

RESULT 12

US-11-060-756-197597/c
; Sequence 197597, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mount, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197597
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-197597

Query Match 72.2%; Score 13; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCCTCTTGGA 15
| | | | | | | | | |
| | | | | | | | | |
Db 18 CCCCTCTTGGA 6

RESULT 13

US-11-060-756-197598/c
; Sequence 197598, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mount, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197598
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-197598

Query Match 72.2%; Score 13; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCCTCTTGGA 15
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| | | | | | | | | |
Db 18 CCCCTCTTGGA 6

RESULT 14

US-10-459-876-17
; Sequence 17, Application US/10459876
; Publication No. US20030208060A1
; GENERAL INFORMATION:
; APPLICANT: Glanturco, S.H.
; APPLICANT: Bradley, W.A.
; TITLE OF INVENTION: DNA Encoding Human apob48R: A Monocyte-Macrophage
; TITLE OF INVENTION: Apolipoprotein B48 Receptor Gene and Protein
; FILE REFERENCE: D5880CIP

; CURRENT APPLICATION NUMBER: US/10/459,876
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US/09/583,610
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/130,242
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense primers were based on the 5'-end
; OTHER INFORMATION: sequence of the THP-1 (73 clone) (bp 2203-2187
US-10-459-876-17

Query Match 66.7%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTCTGGAT 16
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| | | | | | | | | |
Db 5 CCTCTCTGGAT 16

RESULT 15

US-10-659-948A-6/c
; Sequence 6, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovane, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-659-948A-6

Query Match 66.7%; Score 12; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCTGATAC 18
| | | | | | | | | |
| | | | | | | | | |
Db 18 TCTTCTGATAC 7

Search completed: April 7, 2006, 09:17:27
Job time : 350.784 secs